

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:29 ; Search time 121.5 Seconds
(without alignments)
22.282 Million cell updates/sec

Title: SEQ60

Perfect score: 7

Sequence: 1 vmxvae 7

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 7

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	3 AAB07871	Aab07871 A beta-se
2	7	100.0	8	3 AAB07872	Aab07872 A beta-se
3	7	100.0	450	7 ADF06975	Adf06975 Bacterial
4	7	100.0	457	8 ADN46338	Adn46338 Thermococ
5	7	100.0	821	2 AAY34479	Aay34479 Porphorym
6	7	100.0	869	2 AAY34354	Aay34354 Porphorym

ALIGNMENTS

RESULT 1

AAB07871

ID AAB07871 standard; peptide; 7 AA.

AC AAB07871;

XX

XX 14-NOV-2000 (first entry)

XX

XX A beta-secretase inhibitor peptide.

XX

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

XX

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 3 /note= "hydroxyethylene"

FT

XX

PN WO200047618-A2.

XX

XX 17-AUG-2000.

XX

XX 10-FEB-2000; 2000WO-US003819.

XX

XX 10-FEB-1999; 99US-0119571P.

PR

XX 15-JUN-1999; 99US-0139172P.

XX

XX (ELAN-) ELAN PHARM INC.

PA

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;

PI

XX WPI; 2000-533011/48.

DR

XX

XX Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.

PT

XX Disclosure; Page 12; 121pp; English.

XX

XX The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7

DB 1 VMXVAEF 7

|||||

RESULT 2

AAB07872

ID AAB07872 standard; peptide; 8 AA.

XX

XX AAB07872;

XX

XX 14-NOV-2000 (first entry)

XX

XX A beta-secretase inhibitor peptide.

XX

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

XX Synthetic.

OS

XX Key Location/Qualifiers

FT Modified-site 4 /note= "hydroxyethylene"

FT

XX

PN WO200047618-A2.

XX

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US003819.
 PF
 XX
 PR 10-FEB-1999; 99US-0119571P.
 PR 15-JUN-1999; 99US-0139172P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA
 PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
 XX WPI; 2000-533011/48.
 XX
 XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 XX
 XX Disclosure; Page 12; 121pp; English.
 PS
 XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents an inhibitor of beta-secretase enzyme
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 7; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.0e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VMXVAEF 7
 DB |||||
 2 VMXVAEF 8
 RESULT 3
 ADF06975
 ID ADF06975 standard; protein; 450 AA.
 XX
 AC ADF06975;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX Bacterial polypeptide #3088.
 DE
 XX
 XX Proteus mirabilis infection; bacterial infection; antibacterial;
 KW immunostimulant.
 KW
 XX Proteus mirabilis.
 OS
 XX US6605709-B1.
 PN
 XX 12-AUG-2003.
 PD
 XX
 XX 05-APR-2000; 2000US-00543681.
 PF
 XX
 XX 09-APR-1999; 99US-0128706P.
 PR
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Breton GI;
 PI
 XX WPI; 2003-895291/82.
 DR N-PSDB; ADF02803.
 XX
 XX New Proteus mirabilis polypeptides and polynucleotides, useful as
 PT reagents for diagnosis of bacterial disease, as components of

PT antibacterial vaccines, as targets for antibacterial drugs, or as
 PT biocontrol agents for plants.
 XX
 PS Disclosure; SEQ ID NO 7260; 870pp; English.
 XX
 CC The invention relates to new Proteus mirabilis polypeptides and
 CC polynucleotides. The invention also relates to antibodies against the
 CC polypeptides, methods for producing the polypeptides, a method of
 CC generating vaccines for immunising an individual against P. mirabilis, a
 CC method for evaluating a compound for the ability to bind a P. mirabilis
 CC polypeptide and a method for screening test compounds for anti-bacterial
 CC activity. The polypeptides and polynucleotides are useful as molecular
 CC targets for diagnosing, preventing and treating pathological conditions
 CC resulting from bacterial infection, as reagents for diagnosis of
 CC bacterial diseases, as components of antibacterial vaccines, as targets
 CC for antibacterial drugs or as bio-control agents for plants. This
 CC sequence represents a Proteus mirabilis polypeptide of the invention.
 XX
 XX Sequence 450 AA;
 SQ
 Query Match 100.0%; Score 7; DB 7; Length 450;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VMXVAEF 7
 DB |||||
 286 VMXVAEF 292
 RESULT 4
 ADN46338
 ID ADN46338 standard; protein; 457 AA.
 XX
 AC ADN46338;
 XX
 XX 01-JUL-2004 (first entry)
 DT
 XX Thermococcus kodakaraensis KOD1 protein sequence SeqID216.
 DE
 XX gene disruption; gene targeting; marker gene; transformation;
 KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
 KW gene structure; gene function; enzyme activity; medicine;
 KW forensic science; food; drug inspection; molecular biology; immunology.
 XX
 OS Thermococcus kodakaraensis.
 XX
 XX WO2004022736-A1.
 PN
 XX 18-MAR-2004.
 PD
 XX 29-AUG-2003; 2003WO-IB003597.
 PF
 XX 30-AUG-2002; 2002JP-00319011.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Imanaka T, Atomi H;
 PI
 XX WPI; 2004-257583/24.
 DR
 XX Method for disrupting targeted gene in genome of organism particularly
 PT thermostable bacterium and with genome chips for analysis, applicable in
 PT studying gene structure and functions.
 XX
 PS Claim 9; SEQ ID NO 216; 598pp; Japanese.
 XX
 CC This invention relates to a novel method for targeting disruption of an
 CC arbitrary gene in a genome of an organism which comprises providing the
 CC whole sequential data of the genome of such organism, selecting at least
 CC 1 arbitrary region in the sequence, providing a vector that contains a
 CC sequence homologous with the selected region and a marker gene,
 CC transformation, and homologous recombination. The genome is preferably
 CC the genome of a hyperthermostable archaeobacterium, particularly

CC Thermococcus kodakaraensis KOD1. The method is for targeting the
 CC disruption of a gene in the genome of an organism, which is applicable in
 CC studying gene structure and functions as well as enzyme activities of
 CC encoded proteins and useful in medicine, forensic science, food or drug
 CC inspection, molecular biology and immunology. With this method, the
 CC disruption of a gene at an arbitrary position in a genome can be achieved
 CC efficiently and reliably. The present sequence is that of a protein
 CC encoded by the genome of Thermococcus kodakaraensis which was derived
 CC using the method of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 457 AA;

Query Match 100.0%; Score 7; DB 8; Length 457;
 Best Local Similarity 85.7%; Pred. NO. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
 ||:||||
 Db 1 VMEVAEF 7

RESULT 5
 AAY34479
 ID AAY34479 standard; protein; 821 AA.

XX
 AC AAY34479;

DT 27-AUG-2003 (revised)
 DT 20-MAR-2003 (revised)
 DT 25-AUG-1999 (first entry)

XX Porphyromonas gingivalis protein PG21.

XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
 KW antigenic.

OS Porphyromonas gingivalis.

XX WO9929870-A1.

XX 17-JUN-1999.

XX 10-DEC-1998; 98WO-AU001023.

XX 10-DEC-1997; 97AU-00000839.

XX 31-DEC-1997; 97AU-00001182.

XX 30-JAN-1998; 98AU-00001546.

XX 10-MAR-1998; 98AU-00002264.

XX 09-APR-1998; 98AU-00002911.

XX 23-APR-1998; 98AU-00003128.

XX 05-MAY-1998; 98AU-00003338.

XX 22-MAY-1998; 98AU-00003654.

XX 29-JUL-1998; 98AU-00004917.

XX 30-JUL-1998; 98AU-00004963.

XX 04-AUG-1998; 98AU-00005028.

XX (CSLC-) CSL LTD.

XX Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;

XX Hocking DM, Webb EA;

XX WPI; 1999-385613/32.

XX N-PSDB; AAX91697.

XX Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.

XX Claim 1; Page 460-461; 588pp; English.

XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic

CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to

CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 821 AA;

Query Match 100.0%; Score 7; DB 2; Length 821;

Best Local Similarity 85.7%; Pred. NO. 1.9e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
 ||:||||
 Db 565 VMPVAEF 571

RESULT 6
 AAY34354

ID AAY34354 standard; protein; 869 AA.

XX AAY34354;

XX 27-AUG-2003 (revised)

DT 20-MAR-2003 (revised)

DT 25-AUG-1999 (first entry)

XX Porphyromonas gingivalis protein PG21.

XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
 KW antigenic.

OS Porphyromonas gingivalis.

XX WO9929870-A1.

XX 17-JUN-1999.

XX 10-DEC-1998; 98WO-AU001023.

XX 10-DEC-1997; 97AU-00000839.

XX 31-DEC-1997; 97AU-00001182.

XX 30-JAN-1998; 98AU-00001546.

XX 10-MAR-1998; 98AU-00002264.

XX 09-APR-1998; 98AU-00002911.

XX 23-APR-1998; 98AU-00003128.

XX 05-MAY-1998; 98AU-00003338.

XX 22-MAY-1998; 98AU-00003654.

XX 29-JUL-1998; 98AU-00004917.

XX 30-JUL-1998; 98AU-00004963.

XX 04-AUG-1998; 98AU-00005028.

XX (CSLC-) CSL LTD.

XX Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;

XX Hocking DM, Webb EA;

XX WPI; 1999-385613/32.

XX N-PSDB; AAX91572.

XX Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.

XX Claim 1; Page 316-318; 588pp; English.

XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic

CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to

CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the

CC isolation of the PG polypeptides. The PG polypeptides have antibacterial

CC activity with a vaccine mechanism of action. The PG polypeptides can be

CC used as vaccines especially against Porphyromonas gingivalis. Probes can

CC be used to detect Porphyromonas gingivalis in standard hybridisation
CC assays. Porphyromonas gingivalis is involved in periodontal disease
CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 869 AA;

Query Match 100.0%; Score 7; DB 2; Length 869;

Best Local Similarity 85.7%; Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7

||:||||

Db 613 VMPVAEF 619

Search completed: November 15, 2005, 10:54:46

Job time : 121.5 secs

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OM protein - protein search, using sw model
Run on: November 15, 2005, 10:50:30 ; Search time 29.5 Seconds
(without alignments)
17.713 Million cell updates/sec

Title: SEQ60
Perfect score: 7
Sequence: 1 vmxvae7

Scoring table: OLIGODX
Gapop 60.0 , Gapext 60.0
Searched: 513545 seqs, 74649064 residues

Word size : 7
Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-724-566A-78 Sequence 78, Appl
2	7	100.0	7	4	US-09-471-669A-78 Sequence 78, Appl
3	7	100.0	8	4	US-09-724-566A-81 Sequence 81, Appl
4	7	100.0	8	4	US-09-471-669A-81 Sequence 81, Appl
5	7	100.0	450	4	US-09-543-681A-7260 Sequence 7260, Ap

ALIGNMENTS

RESULT 1
US-09-724-566A-78
; Sequence 78, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribail
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-78

Query Match 100.0%; Score 7; DB 4: Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 1 VMXVAEF 7
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RESULT 2
US-09-471-669A-78
; Sequence 78, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribail
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: Inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Xaa is hydroxyethylene or statine

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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:55:49 ; Search time 117 Seconds
(without alignments)
25.033 Million cell updates/sec

Title: SEQ60

Perfect score: 7

Sequence: 1 vmxvaeaf 7

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 7

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	20	US-11-089-918-78
2	7	100.0	7	20	US-11-090-866-78
3	7	100.0	7	20	US-11-069-377-78
4	7	100.0	7	20	US-11-090-872-78
5	7	100.0	7	20	US-11-090-399-78
6	7	100.0	8	20	US-11-089-918-81
7	7	100.0	8	20	US-11-090-866-81
8	7	100.0	8	20	US-11-069-377-81
9	7	100.0	8	20	US-11-090-872-81
10	7	100.0	8	20	US-11-090-399-81

ALIGNMENTS

RESULT 1
US-11-089-918-78
; Sequence 78, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-089-918-78

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
DB 1 VMXVAEF 7

RESULT 2
US-11-090-866-78
; Sequence 78, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

```
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-866-78
```

```
Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VMXVAEF 7
Db 1 VMXVAEF 7
|||||
```

```
RESULT 3
US-11-069-377-78
; Sequence 78, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-069-377-78
```

```
Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VMXVAEF 7
Db 1 VMXVAEF 7
|||||
```

```
RESULT 4
US-11-090-872-78
; Sequence 78, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-872-78
```

```
Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VMXVAEF 7
Db 1 VMXVAEF 7
|||||
```

RESULT 5

```

US-11-090-399-78
; Sequence 78, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-399-78
Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 1 VMXVAEF 7

RESULT 6
US-11-089-918-81
; Sequence 81, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918

```

```

; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-089-918-81
Query Match 100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 2 VMXVAEF 8

RESULT 7
US-11-090-866-81
; Sequence 81, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V

```

```

; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-866-81

Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 2 VMXVAEF 8

RESULT 8
US-11-069-377-81
; Sequence 81, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-12-24
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-069-377-81

Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 2 VMXVAEF 8

RESULT 9
US-11-090-872-81
; Sequence 81, Application US/11090872
; Publication No. US2005017788A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.

```

```

; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-872-81

Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
Db 2 VMXVAEF 8

RESULT 10
US-11-090-399-81
; Sequence 81, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10

```



```

; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 4 _RES
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-399-81

```

```

Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMXVAEF 7
        |||||
Db       2 VMXVAEF 8

```

Search completed: November 15, 2005, 11:18:15
Job time : 117 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:29 ; Search time 24 seconds
(without alignments)
28.063 Million cell updates/sec

Title: SEQ60

Perfect score: 7

Sequence: 1 vmxvae7

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	2638	1 A42545	genome polypeptide

ALIGNMENTS

RESULT 1
A42545
genome polypeptide - Langat virus (strain TP21) (fragment)
N; Contains: nonstructural protein NS1, nonstructural protein NS2a, nonstructural protein NS5
C; Species: Langat virus
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C; Accession: A42545; A61409; C61409
R; Iacono-Connors, L.C.; Schmaljohn, C.S.
Virology 188, 875-880, 1992
A; Title: Cloning and sequence analysis of the genes encoding the nonstructural proteins
A; Reference number: A42545; MUID: 92263794; PMID: 1316684
A; Accession: A42545
A; Molecule type: genomic RNA
A; Residues: 1-2638 <IAC>
A; Cross-references: UNIPROT: P29837; GB: S35365; NID: g249315; PIDN: AAB22165.1; PID: g249316
R; Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Griesikova, M.
J. Gen. Virol. 72, 333-338, 1991
A; Title: The relationship between the flaviviruses Skalica and Langat as revealed by morphological and electron microscopic studies
A; Reference number: A61409; MUID: 91132129; PMID: 1847173
A; Accession: A61409
A; Status: not compared with conceptual translation
A; Molecule type: genomic RNA

A; Residues: 319-337 <GUI>
A; Accession: C61409
A; Status: not compared with conceptual translation
A; Molecule type: genomic RNA
A; Residues: 877-994 <GU2>
C; Superfamily: yellow fever virus genome polypeptide
C; Keywords: glycoprotein; nonstructural protein NS1 #status predicted <NS1>
F; 1-352/Product: nonstructural protein NS2a #status predicted <NS2a>
F; 353-582/Product: nonstructural protein NS2b #status predicted <NS2b>
F; 583-713/Product: nonstructural protein NS3 #status predicted <NS3>
F; 714-1334/Product: nonstructural protein NS4a #status predicted <NS4a>
F; 912-919/Region: nucleotide-binding motif A (P-loop)
F; 1335-1483/Product: nonstructural protein NS4b #status predicted <NS4b>
F; 1484-1735/Product: nonstructural protein NS5 #status predicted <NS5>
F; 1736-2638/Product: nonstructural protein NS5 (covalent) #status predicted <NS5>
F; 85,207,223,873,1212,1671,1950/Binding site: carbohydrate (Asn) (covalent) #status predicted <NS5>

Query Match 100.0%; Score 7; DB 1; Length 2638;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
DB 153 VMTVAEF 159
||:||||

Search completed: November 15, 2005, 10:55:40
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:30 ; Search time 114 Seconds
(without alignments)
31.443 Million cell updates/sec

Title: SEQ60
Perfect score: 7
Sequence: 1 vmxvaeaf 7

Scoring table: OLIGODX
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 7

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	7	100.0	776	2 Q941L7	Q941L7 populus tre
2	7	100.0	821	2 Q9XBW4	Q9XBW4 porphyromon
3	7	100.0	3414	1 POLG.LANVT	P29837 l genome po
4	7	100.0	3414	2 Q9IG39	Q9IG39 langat viru
5	7	100.0	3414	2 Q9IG40	Q9IG40 langat viru

ALIGNMENTS

RESULT 1
Q941L7 PRELIMINARY; PRT; 776 AA.
AC Q941L7
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Putative high-affinity potassium uptake transporter.
GN Names=kupl;
OS Populus tremula x Populus tremuloides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids I; Malpighiales; Salicaceae; Salicaceae; Populus.
OX NCBI_TaxID=47664;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22381938; PubMed=12492841;
RA Langer K., Ache P., Geiger D., Stinzling A., Arend M., Wind C.,
RA Regan S., Fromm J., Hedrich R.;
RT "Poplar potassium transporters capable of controlling K homeostasis
and K dependent xylogenesis.";

RL Plant J. 32:997-1009(2002).
DR EMBL; AJ299422; CAC39168.1; -
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0015079; P.potassium ion transporter activity; IEA.
DR GO; GO:0006813; P.potassium ion transport; IEA.
DR InterPro; IPR003855; K+ transporter.
DR Pfam; PF02705; K trans; 1.
DR TIGRFAMs; TIGR00794; kup; 1.
SQ SEQUENCE 776 AA; 87303 MW; BEC03D57ED0869BC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 776;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
DB 604 VMSVAEF 610

RESULT 2

Q9XBW4 PRELIMINARY; PRT; 821 AA.
AC Q9XBW4; Q7BWB5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Immunoreactive 92 kDa antigen PG21 (Zinc carboxypeptidase, putative).
GN OrderedLocusNames=PG0232;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W50;
RA Ross B.C., Barr I., Patterson M., Agius C., Rothe L., Margetta M.,
RA Hocking D., Webb E.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL; AF153768; AAD38980.1; -
DR EMBL; AE017172; AAQ65462.1; -
DR HSSP; Q90240; 1QMU.
DR MEROPS; M14.023; -
DR TIGR; PG0232; -
DR GO; GO:0004182; F.carboxypeptidase A activity; IEA.
DR GO; GO:0008270; F.zinc ion binding; IEA.
DR GO; GO:0006508; P.proteolysis and peptidolysis; IEA.
DR InterPro; IPR008969; Carboxypep reg.
DR InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00246; Peptidase_M14; 1.
DR Pfam; PF00801; PKD; 3.
DR PRINTS; PR00765; CRBOXYPTASEA.
DR SMART; SM00089; PKD; 3.
DR SMART; SM0631; Zn_pept; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
DR PROSITE; PS50093; PKD; 3.
KW Complete proteome.
SQ SEQUENCE 821 AA; 91517 MW; 250843B2C9C833B2 CRC64;

```

Query Match          100.0%; Score 7; DB 2; Length 821;
Best Local Similarity 85.7%; Pred. NO. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMKVAEF 7
Db      565 VMPVAEF 571

RESULT 3
POLG LANVT          STANDARD;          PRT; 3414 AA.
AC P29837;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Genome polypeptide [Contains: Capsid protein C (Core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2A, NS2B, NS4A and NS4B; Flavivirin (EC 3.4.21.91)
DE (NS2B/NS3 proteinase) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
DE (NS5)].
OS Langkat virus (strain TP21).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=31638;
RN [1]
RP SEQUENCE OF 1-776 FROM N.A.
RX MEDLINE=92074260; PubMed=1720591;
RA Mandl C.W., Iacono-Connors L., Wallner G., Holzmann H., Kunz C.,
RA Heinz F.X.;
RT "Sequence of the genes encoding the structural proteins of the low-
RT virulence tick-borne flaviviruses Langkat TP21 and Yelantsev.";
RL Virology 185:891-895 (1991).
RN [2]
RP SEQUENCE OF 777-3414 FROM N.A.
RX MEDLINE=92263794; PubMed=1316684;
RA Iacono-Connors L.C., Schmaljohn C.S.;
RT "Cloning and sequence analysis of the genes encoding the nonstructural
RT proteins of Langkat virus and comparative analysis with other
RT flaviviruses.";
RL Virology 188:875-880 (1992).
CC -!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic,
CC suggesting a possible membrane-related function. NS5 may play a
CC role in the viral RNA replication. NS3 and NS2B form a protease
CC which processes the viral polyprotein into separate proteins.
CC -!- CATALYTIC ACTIVITY: Selective hydrolysis of xaa-xaa-|-xbb bonds in
CC which each of the xaa can be either arg or lys and xbb can be
CC either ser or ala.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a
CC lipoprotein envelope. The envelope consists of two proteins:
CC protein M and glycoprotein E. The nucleocapsid is a complex of
CC protein C and mRNA. In immature particles, there are 60
CC icosahedrally organized trimeric spikes on the surface. Each spike
CC consists of three heterodimers of envelope protein M precursor
CC (prM) and envelope protein E (By similarity).
CC -!- SIMILARITY: Contains 1 peptidase S7 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73835; AAA02740.1; AUT_TERM.
CC EMBL; S35365; AAB22165.1; -.
CC FIR; A42545; A42545.
CC HSP; P14336; 1SVB.
CC MEROPS; S07.001; -.
CC InterPro; IPR001410; DEAD.

```

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DR InterPro; IPR002464; DEAD_box.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR001157; Flavi_NS1.
DR InterPro; IPR000752; Flavi_NS2A.
DR InterPro; IPR000487; Flavi_NS2B.
DR InterPro; IPR000404; Flavi_NS4A.
DR InterPro; IPR001528; Flavi_NS4B.
DR InterPro; IPR000208; Flavi_NS5.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001850; Peptidase_S7.
DR InterPro; IPR007095; RNA_pol_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR002877; RrmJftsJ_mfrase.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF00948; Flavi_NS1; 1.
DR Pfam; PF01005; Flavi_NS2A; 1.
DR Pfam; PF01002; Flavi_NS2B; 1.
DR Pfam; PF01350; Flavi_NS4A; 1.
DR Pfam; PF01349; Flavi_NS4B; 1.
DR Pfam; PF00972; Flavi_NS5; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PF01728; FtsJ; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00949; Peptidase_S7; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
DR ProDom; PD001496; Flavi_NS1; 1.
DR ProSITE; PS00690; DEAD_ATP_HELICASE; FALSE NEG.
KW ATP-binding; Coat protein; Core protein; Core protein; Envelope protein;
KW Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
KW RNA-directed RNA polymerase; Transferrase; Transmembrane.
FT INIT_MET 1 1
FT CHAIN 1 112
FT PROPEP 113 205
FT CHAIN 206 280
FT CHAIN 281 776
FT CHAIN 777 1128
FT CHAIN 1129 1358
FT CHAIN 1359 1489
FT CHAIN 1490 2110
FT CHAIN 2111 2259
FT CHAIN 2260 2511
FT CHAIN 2512 3414
FT NP_BIND 1688 1695
FT ACT_SITE 1543 1543
FT ACT_SITE 1567 1567
FT ACT_SITE 1627 1627
FT SITE 1779 1782
FT TRANSMEM 103 119
FT TRANSMEM 262 278
FT TRANSMEM 728 744
FT TRANSMEM 758 774
FT DISULFID 283 310
FT DISULFID 340 396
FT DISULFID 354 385
FT DISULFID 372 401
FT DISULFID 466 570
FT DISULFID 587 618
FT CARBOHYD 144 144
FT CARBOHYD 434 434
SQ SEQUENCE 3414 AA; 378017 MW; 59CB7E95DD70D82E CRC64;

Query Match          100.0%; Score 7; DB 1; Length 3414;
Best Local Similarity 85.7%; Pred. NO. 7.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 1 VMXVAEP 7
Db 929 VMTVAEP 935

RESULT 4
Q9IG39 PRELIMINARY; PRT; 3414 AA.
AC Q9IG39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein precursor.
OS Langat virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=attenuated strain E5;
RX MEDLINE=20192178; PubMed=1075214; DOI=10.1006/viro.2000.0220;
RA Campbell M.S., Pletnev A.G.;
RT "Infectious cDNA clones of Langat tick-borne flavivirus that differ
from their parent in peripheral neurovirulence.";
RL Virology 269:225-237(2000).
DR EMBL; AF253420; AAF75360.1; -.
DR HSSP; P14336; 1SVB.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR01122; Flavi_capsidC.
DR InterPro; IPR011492; Flavi_DEAD.
DR InterPro; IPR000336; Flavi_Glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR001157; Flavi_NS1.
DR InterPro; IPR000752; Flavi_NS2A.
DR InterPro; IPR000487; Flavi_NS2B.
DR InterPro; IPR000404; Flavi_NS4A.
DR InterPro; IPR001528; Flavi_NS4B.
DR InterPro; IPR00208; Flavi_NS5.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001850; Peptidase_S7.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR002877; RmJftsJ_mtfase.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF07652; Flavi_DEAD; 1.
DR Pfam; PF00869; Flavi_Glycoprot; 1.
DR Pfam; PF02832; Flavi_Glycop_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF00948; Flavi_NS1; 1.
DR Pfam; PF01005; Flavi_NS2A; 1.
DR Pfam; PF01002; Flavi_NS2B; 1.
DR Pfam; PF01350; Flavi_NS4A; 1.
DR Pfam; PF01349; Flavi_NS4B; 1.
DR Pfam; PF00972; Flavi_NS5; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PF01728; FtsJ; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00949; Peptidase_S7; 1.
DR ProDom; PD001556; Flavi_Glycoprote; 1.
DR ProDom; PD001496; Flavi_NS1; 1.

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DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW ATP-binding; Helicase; Hydrolase; Polyprotein; Signal.
FT SIGNAL 97 116 Potential.
FT CHAIN 780 1128 nonstructural protein NS1.
FT CHAIN 1129 1358 nonstructural protein NS2a.
FT CHAIN 1359 1489 nonstructural protein NS2b.
FT CHAIN 1490 2110 nonstructural protein NS3.
FT CHAIN 2111 2259 nonstructural protein NS4a.
FT CHAIN 2260 2511 nonstructural protein NS4b.
FT CHAIN 117 280 membrane-associated glycoprotein precursor.
FT CHAIN 2512 3414 nonstructural protein NS5.
FT CHAIN 281 779 envelope membrane-associated glycoprotein.
FT CHAIN 1 96 capsid protein.
SQ SEQUENCE 3414 AA; 378018 MW; BF8F8ACEAB96D534 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 3414;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMXVAEP 7
Db 929 VMTVAEP 935

RESULT 5
Q9IG40 PRELIMINARY; PRT; 3414 AA.
AC Q9IG40;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein precursor.
OS Langat virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TP21;
RX MEDLINE=20192178; PubMed=1075214; DOI=10.1006/viro.2000.0220;
RA Campbell M.S., Pletnev A.G.;
RT "Infectious cDNA clones of Langat tick-borne flavivirus that differ
from their parent in peripheral neurovirulence.";
RL Virology 269:225-237(2000).
DR EMBL; AF253419; AAF75259.1; -.
DR FIR; B41704; B41704.
DR HSSP; P14336; 1SVB.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR011492; Flavi_DEAD.
DR InterPro; IPR000336; Flavi_Glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR001157; Flavi_NS1.
DR InterPro; IPR000752; Flavi_NS2A.
DR InterPro; IPR000487; Flavi_NS2B.
DR InterPro; IPR000404; Flavi_NS4A.
DR InterPro; IPR001528; Flavi_NS4B.
DR InterPro; IPR00208; Flavi_NS5.
DR InterPro; IPR002535; Flavi_propep.

```

DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001850; Peptidase_S7.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR002877; RrmJFtsJ_mfrase.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF07652; Flavi_DEAD; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF00948; Flavi_NS1; 1.
DR Pfam; PF01005; Flavi_NS2A; 1.
DR Pfam; PF01002; Flavi_NS2B; 1.
DR Pfam; PF01350; Flavi_NS4A; 1.
DR Pfam; PF01349; Flavi_NS4B; 1.
DR Pfam; PF00972; Flavi_NS5; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PF01728; FtsJ; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00949; Peptidase_S7; 1.
DR ProDom; PD001556; Flavi_glycoprotE; 1.
DR ProDom; PD001496; Flavi_NS1; 1.
DR SMART; SM00487; DEXDc; 1.
DR SMART; SM00490; HELICc; 1.
KW ATP-binding; Helicase; Hydrolase; Polypeptin; Signal.
FT SIGNAL 97 116 Potential.
FT CHAIN 780 1128 nonstructural protein NS1.
FT CHAIN 1129 1358 nonstructural protein NS2a.
FT CHAIN 1359 1489 nonstructural protein NS2b.
FT CHAIN 1490 2110 nonstructural protein NS3.
FT CHAIN 2111 2259 nonstructural protein NS4a.
FT CHAIN 2260 2511 nonstructural protein NS4b.
FT CHAIN 117 280 membrane-associated glycoprotein precursor.
FT CHAIN 2512 3414 nonstructural protein NS5.
FT CHAIN 281 779 envelope membrane-associated glycoprotein.
FT CHAIN 1 96 capsid protein.
SQ SEQUENCE 3414 AA; 378138 MW; 8DE86A46A0E8F7E3 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 3414;
Best Local Similarity 85.7%; Pred.No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMXVAEF 7
||:||||
Db 929 VMTVAEF 935

Search completed: November 15, 2005, 10:59:37
Job time : 115 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:29 ; Search time 121.5 Seconds
(without alignments)
22.282 Million cell updates/sec

Title: SEQ59

Perfect score: 7
Sequence: 1 vxxxaef 7

Scoring table: OLIGODX
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 7

Total number of hits satisfying chosen parameters: 3251

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	3 AAB07871	Aab07871 A beta-se
2	7	100.0	7	4 AAB61347	Aab61347 Peptide O
3	7	100.0	7	4 AAB66585	Aab66585 Human mem
4	7	100.0	7	5 AAB78390	Abg78390 Memapsin
5	7	100.0	7	5 AAE19124	Aae19124 Beta-secr
6	7	100.0	7	5 AAU99502	Aau99502 Human mem
7	7	100.0	7	6 AABG75988	Abg75988 Amyloid p
8	7	100.0	7	6 AABG76114	Abg76114 Synthetic
9	7	100.0	7	6 ADA74842	Ada74842 OM99-1 pe
10	7	100.0	7	7 ADM78547	Adm78547 Protease
11	7	100.0	7	8 ADJ71544	Adj71544 N-termina
12	7	100.0	7	8 ADS09464	Ads09464 Beta-secr
13	7	100.0	8	3 AAY94771	Aay94771 Beta-secr
14	7	100.0	8	3 AAY94772	Aay94772 Beta-secr
15	7	100.0	8	3 AAY94773	Aay94773 Beta-secr
16	7	100.0	8	3 AAB07872	Aab07872 A beta-se
17	7	100.0	8	4 AAU07230	Aau07230 Human bet
18	7	100.0	8	4 AAE10661	Aae10661 Human asp
19	7	100.0	8	4 AAE10660	Aae10660 Human asp
20	7	100.0	8	4 AAE06902	Aae06902 Human amy
21	7	100.0	8	4 AAB61348	Aab61348 Peptide O
22	7	100.0	8	4 AAE02613	Aae02613 Human Asp
23	7	100.0	8	4 AAE02612	Aae02612 Human Asp
24	7	100.0	8	4 AAB66586	Aab66586 Human mem
25	7	100.0	8	4 AAB97467	Aab97467 Asp2 inhi

ALIGNMENTS

RESULT 1

AAB07871
ID AAB07871 standard; peptide; 7 AA.

XX AC AAB07871;

XX DT 14-NOV-2000 (first entry)

XX DE A beta-secretase inhibitor peptide.

XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 3 /note= "hydroxyethylene"

XX PN WO200047618-A2.

XX PD 17-AUG-2000.

XX PF 10-FEB-2000; 2000WO-US003819.

XX PR 10-FEB-1999; 99US-0119571P.

XX PR 15-JUN-1999; 99US-0139172P.

XX PA (ELAN-) ELAN PHARM INC.

XX PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

XX PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;

XX DR WPI; 2000-533011/48.

XX PT Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g.

XX PT Alzheimer's disease.

XX PS Disclosure; Page 12; 12ipp; English.

XX CC The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-

CC Like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents an inhibitor of beta-secretase enzyme

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 1 VMXAAEF 7

RESULT 2

AAB61347
 ID AAB61347 standard; peptide; 7 AA.

XX AC AAB61347;

XX DT 02-APR-2001 (first entry)

XX DE Peptide OM99-1.

XX KW Memapsin 2; catalyst; Alzheimer's.

XX OS Unidentified.

XX PN WO200100663-A2.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-US017661.

XX PR 28-JUN-1999; 99US-0141363P.

XX PR 30-NOV-1999; 99US-0168060P.

XX PR 25-JAN-2000; 2000US-0177836P.

XX PR 27-JAN-2000; 2000US-0178368P.

XX PR 08-JUN-2000; 2000US-0210292P.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Tang JUN, Lin X, Koelsch G;

XX DR WPI; 2001-102885/11.

XX PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease.

XX PS Example 7; Page 36; 86pp; English.

XX CC The present invention relates to a purified recombinant catalytically
 CC active memapsin 2. The invention may be used for isolating inhibitors
 CC which are used to treat or prevent Alzheimer's disease. The invention may
 CC also be used to screen for individuals more genetically prone to develop
 CC Alzheimer's disease

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 1 VNLADEF 7

RESULT 3

AAB66585

ID AAB66585 standard; peptide; 7 AA.
 XX AC AAB66585;
 XX DT 12-APR-2001 (first entry)
 XX DE Human memapsin 2 inhibitor OM99-1.
 XX KW Human memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
 KW APP; memapsin 2 inhibitor; Alzheimer's disease.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 3..4
 FT /note= "residues 3 and 4 form a Leu-Ala dipeptide
 FT isotere"

XX PN WO200100665-A2.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-US017742.

XX PR 28-JUN-1999; 99US-0141363P.

XX PR 30-NOV-1999; 99US-0168060P.

XX PR 25-JAN-2000; 2000US-0177836P.

XX PR 27-JAN-2000; 2000US-0178368P.

XX PR 08-JUN-2000; 2000US-0210292P.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI (UNII) UNIV ILLINOIS FOUND.

XX PI Tang JUN, Hong L, Ghosh AK;

XX DR WPI; 2001-137933/14.

XX PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
 PT having 2 catalytic aspartic residues and substrate binding cleft, used to
 PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.

XX PS Example 7; Page 36; 86pp; English.

XX CC The present sequence is given in a specification relating to an inhibitor
 CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
 CC active site, which is defined by the presence of two catalytic aspartic
 CC residues and a substrate binding cleft. The inhibitor is useful for the
 CC treatment and diagnosis of Alzheimer's disease. It is useful in screens
 CC for individuals with a genetic predisposition to Alzheimer's disease. The
 CC inhibitor is useful as a reagent for specifically binding to memapsin 2
 CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,
 CC purification and characterisation

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 1 VNLADEF 7

RESULT 4

ABG78390
 ID ABG78390 standard; peptide; 7 AA.

XX AC ABG78390;

XX DT 15-NOV-2002 (first entry)

XX DE Memapsin 2 inhibitor OM99-1.

```

XX Memapsin 2; aspartic protease; beta secretase; inhibitor;
KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
KW APP; neuroprotective; nootropic; substrate side-chain preference.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200253594-A2.
XX
PD 11-JUL-2002.
XX
PF 28-DEC-2001; 2001WO-US050826.
XX
PR 28-DEC-2000; 2000US-0258705P.
PR 14-MAR-2001; 2001US-0275756P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII ) UNIV ILLINOIS FOUND.
XX
PI Tang JJN, Koelsch G, Ghosh AK;
XX
DR WPI; 2002-619088/66.
XX
PT New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
PT disease.
XX
PS Example 3; Page 32; 74pp; English.
XX
CC The invention relates to an inhibitor of catalytically active memapsin 2
CC (an aspartic protease which can cleave at beta secretase sites), which
CC binds to the active site of memapsin 2 defined by the presence of two
CC catalytic aspartic residues and substrate binding cleft. Also included is
CC a method of determination of the substrate side-chain preference in
CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
CC substrates with memapsin 2, and determining the sub-site preference of
CC memapsin 2 by determining relative initial hydrolysis rates of the
CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
CC library of memapsin 2 inhibitors containing a base sequence taken from
CC OM99-2 (Glu-Val-Asn-Leu-Ala-Glu-phe), probing the library of
CC inhibitors with memapsin 2 which binds to several inhibitors to generate
CC several bound memapsin 2, and detecting the bound memapsin 2 with an
CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
CC secondary antibody. The inhibitors may be used in the manufacture of a
CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
CC be involved in the cleavage of amyloid precursor protein (APP), and for
CC determining the substrate side-chain preference in memapsin 2 sub-sites.
CC The present sequence represents a potential or actual inhibitor of human
CC memapsin 2
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
DB 1 VNLAEF 7
RESULT 5
AAE19124
ID AAE19124 standard; peptide; 7 AA.
XX
AC AAE19124;
XX
XX 21-MAY-2002 (first entry)
XX
DE Beta-secretase peptide for amyloid precursor protein.
XX
KW Luciferase; enzyme; protease; cell growth; apoptosis; therapeutic;
KW cell death; beta-secretase; amyloid precursor protein.

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XX Unidentified.
OS
PN WO200206458-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022478.
XX
PR 19-JUL-2000; 2000US-00619047.
XX
PA (CHEM-) CHEMICON INT INC.
XX
PI Leng J;
XX
DR WPI; 2002-195809/25.
XX
PT New purified luciferase polypeptide, useful for identifying protease
PT activity modulators, comprises recognition site cleavable by protease,
PT where cleavage of polypeptide results in decreased luciferase activity.
XX
PS Claim 63; Page 24; 56pp; English.
XX
CC The invention relates to a purified polypeptide having luciferase
CC activity and a recognition site specifically cleavable by a protease,
CC where cleavage results in a decrease in luciferase activity. The
CC polypeptide comprises a localisation sequence which is linked to the
CC luciferase polypeptide by the cleavable recognition sequence. The
CC polypeptide is useful for identifying a protease (Caspase-3) activity
CC modulator, an inhibitor of apoptosis and for detecting luciferase
CC activity in a sample. The polypeptide is used for characterising and
CC identifying cellular processes associated with metabolism, cell growth
CC and cell death e.g. apoptosis and for measuring protease activity. The
CC protease measurement methods are useful for characterising, identifying
CC cellular biochemical pathways as well as identifying diagnostic and
CC agents for modulating diseases or disorders associated with biochemical
CC pathways. The polypeptide is also useful as a substrate to study agents
CC or conditions that cleave the recognition site and for determining amount
CC of protease in a sample and for monitoring the activity of protease
CC inside a cell that expresses a recombinant luciferase. The present
CC sequence is beta-secretase peptide for amyloid precursor protein used in
CC the invention
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
DB 1 VKMDAEF 7
RESULT 6
AAU99502
ID AAU99502 standard; peptide; 7 AA.
XX
AC AAU99502;
XX
XX 07-OCT-2002 (first entry)
XX
DE Human memapsin 2 inhibitor, OM99-1.
XX
KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic.
XX
OS Synthetic.
XX
PN US2002049303-A1.
XX
PD 25-APR-2002.

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XX PF 28-FEB-2001; 2001US-00796264.
XX XX
XX PR 28-JUN-1999; 99US-0141363P.
XX PR 30-NOV-1999; 99US-0168060P.
XX PR 25-JAN-2000; 2000US-0177836P.
XX PR 27-JAN-2000; 2000US-0178368P.
XX PR 27-JUN-2000; 2000US-00604608.
XX XX
XX PA (TANG/) TANG J J N.
XX PA (LINK/) LIN X.
XX PA (KOEL/) KOELSCH G.
XX PA (HONG/) HONG L.
XX XX
XX PI Tang JUN, Lin X, Koelsch G, Hong L;
XX XX
XX DR WPI; 2002-507280/54.
XX XX
XX PT New recombinant catalytically active memapsin 2, useful to screen for
XX PT inhibitors of memapsin 2 which can be used to prevent and treat
XX PT Alzheimer's disease.
XX PS Example 7; Page 13; 44pp; English.
XX XX
XX CC The present invention relates to methods for the production of purified,
XX CC recombinant catalytically active, memapsin 2 (beta secretase). Memapsin
XX CC 2, a member of the aspartic protease family, cleaves beta-amyloid
XX CC precursor protein (APP) found in amyloid plaques. The recombinant
XX CC memapsin 2 is useful for identifying inhibitors of memapsin 2 in the
XX CC design of drugs for the treatment and/or prevention of Alzheimer's
XX CC disease. The recombinant memapsin 2 can be used to immunise against
XX CC Alzheimer's disease. The present sequence represents a synthetic
XX CC inhibitor of human memapsin 2
XX XX
XX SQ Sequence 7 AA;
XX XX
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
1 VNLAEEF 7

RESULT 7
ABG75988
ID ABG75988 standard; peptide; 7 AA.
XX AC
XX ABG75988;
XX DT
XX DT 30-APR-2003 (first entry)
XX XX
XX DE Amyloid precursor b-secretase cleavage site.
XX XX
XX KW Green fluorescent protein; GFP; FRGT; protease cleavage site;
XX KW fluorescent resonance energy transfer; tandem fluorescent protein;
XX KW enzymatic assay; Alzheimer's disease; hypertension; inflammation;
XX KW apoptosis; AIDS; acquired immunodeficiency syndrome.
XX XX
XX OS Synthetic.
XX XX
XX FH US2002164674-A1.
XX FT
XX FT 07-NOV-2002.
XX XX
XX PF 25-JAN-2002; 2002US-00057505.
XX XX
XX PR 31-JAN-1996; 96US-00594575.
XX PR 31-JAN-1997; 97US-00792553.
XX PR 13-SEP-1999; 99US-00396003.
XX XX
XX PA (REGC ) UNIV CALIFORNIA.

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XX TSien RY, Heim R, Cubitt A;
XX WPI; 2003-247255/24.
XX XX
XX PT New tandem fluorescent protein construct comprising a donor or acceptor
XX PT fluorescent protein moiety or a linker moiety that couples the donor and
XX PT acceptor moieties, useful in enzymatic assays.
XX XX
XX PS Disclosure; Page 7; 34pp; English.
XX XX
XX CC The invention relates to a tandem fluorescent protein construct
XX CC comprising a donor or acceptor fluorescent protein moiety (e.g. jellyfish
XX CC green fluorescent protein, GFP) or a linker moiety that couples the donor
XX CC and acceptor moieties. Also include are a recombinant nucleic acid coding
XX CC for expression of the tandem fluorescent protein construct, an expression
XX CC vector comprising expression control sequences operatively linked to a
XX CC sequence coding for the expression of the tandem fluorescent protein
XX CC construct, a host cell transfected with the expression vector,
XX CC determining whether a sample contains an enzyme or whether a compound
XX CC alters the activity of an enzyme, determining the amount of activity of
XX CC an enzyme in a cell and testing for cleavage enzyme activity. The tandem
XX CC fluorescent protein construct is useful in enzymatic assays, using the
XX CC principle of fluorescent resonance energy transfer (FRET) between the
XX CC donor and acceptor moieties. The tandem fluorescent proteins are
XX CC particularly useful in assays for protease activity. Proteases play an
XX CC essential role in many disease processes e.g. Alzheimer's disease,
XX CC hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency
XX CC syndrome). Tandem fluorescent proteins were constructed comprising
XX CC mutants of GFP with altered fluorescent spectra. The present sequence
XX CC represents a protease cleavage site which may be incorporated into the
XX CC tandem fluorescent protein construct
XX XX
XX SQ Sequence 7 AA;
XX XX
Query Match 100.0%; Score 7; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
1 VRMDAEF 7

RESULT 8
ABG76114
ID ABG76114 standard; peptide; 7 AA.
XX AC
XX ABG76114;
XX DT
XX DT 01-MAY-2003 (first entry)
XX XX
XX DE Synthetic memapsin 2 inhibitor OM99-1.
XX XX
XX KW Memapsin 2; beta-secretase; beta-amyloid precursor protein;
XX KW beta-amyloid peptide; Alzheimer's disease; neurotropic; neuroprotective;
XX KW substrate analogue; inhibitor; OM99-1.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 3..4
XX FT /label= OTHER
XX FT /note= "The bond between these two residues is a
XX FT transition-state analogue isostere (-CH(OH)-CH2-)"
XX XX
XX PN US2002164760-A1.
XX XX
XX PD 07-NOV-2002.
XX XX
XX PF 28-FEB-2001; 2001US-00795903.
XX XX
XX PR 28-JUN-1999; 99US-0141363P.

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PR 30-NOV-1999; 99US-0168060P.
PR 25-JAN-2000; 2000US-0177836P.
PR 27-JAN-2000; 2000US-0177836P.
PR 08-JUN-2000; 2000US-0210292P.
PR 27-JUN-2000; 2000US-00604608.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Lin X, Koelsch G, Tang JJJ;
XX WPI; 2003-255218/25.
XX
XX New purified recombinant catalytically active memapsin 2 (beta-
XX secretase), useful for designing and screening of specific inhibitors for
XX the diagnosis, prevention and/or treatment of Alzheimer's disease.
XX
XX Example 7; Page 12; 44pp; English.
XX
XX The invention relates to a purified recombinant catalytically active
XX memapsin 2, a beta-secretase which produces the beta-amyloid peptide from
XX the beta amyloid precursor protein. Also included are producing the above
XX memapsin 2 (comprising refolding the recombinant memapsin 2 under
XX conditions which dissociate and then slowly refold the enzyme into a
XX catalytically active form), isolating inhibitors of cleavage by memapsin
XX 2 (comprising adding to one or more potential inhibitors the memapsin 2
XX and a substrate for memapsin 2 and screening for decreased cleavage of
XX the substrate by the inhibitors), designing or obtaining inhibitors of
XX the memapsin 2 (comprising modelling an inhibitor based on the
XX crystallisation coordinates of memapsin 2 or the parameters given in the
XX specification), a database comprising binding properties and chemical
XX structures of compounds designed or screened by the method above and
XX treating or preventing Alzheimer's disease (comprising administering to a
XX patient an inhibitor of memapsin 2 which binds to the active site of the
XX memapsin 2 defined by the presence of 2 catalytic aspartic residues and
XX substrate binding cleft or immunising an individual with the above
XX memapsin 2 to elicit an amount of antibodies to reduce the cleavage by
XX endogenous memapsin 2). The memapsin 2 is useful in designing and
XX screening of specific inhibitors for the diagnosis, prevention and/or
XX treatment of Alzheimer's disease. The present sequence represents a
XX synthetic substrate analogue and inhibitor of memapsin 2
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 7; DB 6; Length 7;
XX Best Local Similarity 57.1%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXAEF 7
XX |::|||
XX 1 VNLAEEF 7
XX
XX Db
XX
XX RESULT 9
XX ADA74842
XX ID ADA74842 standard; peptide; 7 AA.
XX AC
XX ADA74842;
XX
XX 20-NOV-2003 (first entry)
XX
XX OM99-1 peptide inhibitor of human memapsin 2.
XX
XX memapsin 2; beta-secretase; amyloid precursor protein; APP;
XX aspartic proteinase 2; Asp2; nontropic; neuroprotective;
XX Alzheimer's disease; OM99-1 inhibitor.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 3..4
XX /label= OTHER
XX /note= "OTHER = Leu3 and Ala4 linked by a transition-
XX
XX FT

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FT XX state isostere (-CH[OH]-CH2-) "
XX US6545127-B1.
XX 08-APR-2003.
XX
XX 27-JUN-2000; 2000US-00604608.
XX
XX 28-JUN-1999; 99US-0141363P.
XX 30-NOV-1999; 99US-0168060P.
XX 25-JAN-2000; 2000US-0177836P.
XX 27-JAN-2000; 2000US-0178368P.
XX 08-JUN-2000; 2000US-0210292P.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JJJ, Lin X, Koelsch G, Hong L;
XX WPI; 2003-566587/53.
XX
XX Novel memapsin 2 protein that cleaves a beta-secretase site of an amyloid
XX precursor protein is useful in the design and screening of specific
XX inhibitors for treating and preventing Alzheimer's disease.
XX
XX Example 7; Col 22; 44pp; English.
XX
XX The invention relates to a novel method which comprises the production of
XX purified, catalytically active, recombinant memapsin 2 (beta-secretase)
XX protein where the memapsin protein is expressed in a bacterial cell and
XX cleaves the beta-secretase site of an amyloid precursor protein (APP).
XX Memapsin 2, also known as aspartic proteinase 2 (ASP2), belongs to the
XX aspartic protease family and demonstrates nontropic and neuroprotective
XX activities. The protein of the invention may be useful in the design and
XX screening of specific inhibitors which are useful in treating and
XX preventing Alzheimer's disease. The current sequence is that of the OM99-
XX 1 peptide inhibitor of human memapsin 2 of the invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 7; DB 6; Length 7;
XX Best Local Similarity 57.1%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXAEF 7
XX |::|||
XX 1 VNLAEEF 7
XX
XX Db
XX
XX RESULT 10
XX ADM78547
XX ID ADM78547 standard; peptide; 7 AA.
XX AC ADM78547;
XX
XX 03-JUN-2004 (first entry)
XX
XX Protease cleavage recognition site #8.
XX
XX fluorescence; Aequorea green fluorescent protein; GFP.
XX Synthetic.
XX
XX US2003170767-A1.
XX 11-SEP-2003.
XX
XX 12-NOV-2002; 2002US-00293580.
XX
XX 24-JUL-1998; 98US-00129192.
XX (AURO-) AURORA BIOSCIENCES CORP.
XX Cubitt AB;
XX
XX PI

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XX WPI; 2003-863757/80.

XX A fluorescent compound comprising a fluorescent protein moiety and a

PT substrate recognition motif for an activity, which exhibits a change in

PT fluorescence in response to the activity, used to detect enzyme activity

PT in biological samples.

XX

XX Disclosure; SEQ ID NO 44; 52pp; English.

XX

XX The invention relates to a fluorescent compound for detecting an

CC activity, comprising a fluorescent protein moiety and at least one

CC exogenous substrate recognition motif for an activity, where the

CC fluorescent protein moiety can be converted from a first to a second

CC state in response to the activity, and where the fluorescent compound

CC exhibits a different fluorescent property in the two states under

CC quenching conditions. The activity is an enzymatic activity, preferably a

CC kinase, phosphatase, protease, glycosylation or farnesyl transferase

CC activity. The fluorescent protein moiety comprises an Aequorea-related

CC fluorescent protein preferably comprising the mutations in GFP mutant K9,

CC where at least one substrate recognition motif for an activity is within

CC the first 20, more preferably the first 10 amino acids of the amino

CC terminus. The Aequorea-related moiety comprises a poly-Lys region and a

CC protein-protein interaction domain and is membrane bound. The quenching

CC condition is acid quenching. The moiety preferably comprises a

CC phosphorylation recognition motif for a serine/threonine specific protein

CC kinase, protein kinase A, protein kinase C, a cGMP-dependent kinase,

CC Ca2+/calmodulin-dependent protein kinase I or II or MAP kinase activated

CC protein kinase. The compound is used to detect enzymatic activities in

CC biological samples. The present sequence represents a GFP protease

CC cleavage site used in the fluorescent compound of the invention.

XX

XX Sequence 7 AA;

SQ

Query Match 100.0%; Score 7; DB 7; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

Db 1 VKMDAEF 7

RESULT 11

ADJ71544

ID ADJ71544 standard; peptide; 7 AA.

XX

AC ADJ71544;

XX

DT 06-MAY-2004 (first entry)

XX

DE N-terminal APP peptide C-terminal fragment, SEQ ID 207.

XX

XX Nootropic; Neuroprotective; Vaccine; Beta Amyloid;

XX amyloid precursor protein; APP; Alzheimer's disease.

XX

XX Homo sapiens.

OS

XX WO2004013172-A2.

PN

XX 12-FEB-2004.

PD

XX 18-JUL-2003; 2003WO-EP007833.

PF

XX 24-JUL-2002; 2002EP-00447147.

PR

XX 06-AUG-2002; 2002US-0401497P.

PR

XX (INNO-) INNOGENETICS NV.

PA

XX Delacourte A, Sergeant N;

XX

XX WPI; 2004-180423/17.

XX

PT New beta-amyloid or amyloid precursor protein preparation, useful as a

PT prophylactic vaccine or a therapeutic for preventing or treating a

PT disease associated with beta-amyloid formation and/or aggregation, e.g.

PT Alzheimer's disease.

XX

XX Claim 7; Page 67; 104pp; English.

XX

XX The present invention relates to preparations (I) comprising a beta-

CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-

CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal

CC fragment. The beta-amyloid or APP preparations are useful for

CC manufacturing a prophylactic vaccine or a therapeutic, or as a

CC prophylactic vaccine for the prevention, or as a therapeutic for the

CC treatment of a disease associated with beta-amyloid formation and/or

CC aggregation, such as Alzheimer's disease.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 8; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

Db 1 VKMDAEF 7

RESULT 12

ADS09464

ID ADS09464 standard; peptide; 7 AA.

XX

AC ADS09464;

XX

DT 02-DEC-2004 (first entry)

XX

DE Beta-secretase inhibitory peptide - SEQ ID 35.

XX

XX beta-secretase inhibitory peptide; neurodegenerative disease;

XX Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;

XX cerebral palsy; memory loss; SAPPa secretion promoter;

XX neurotropic factor-like agent.

XX

OS Unidentified.

XX

XX Key Location/Qualifiers

FT Modified-site 3

FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"

XX

XX WO2004076478-A1.

PN

XX 10-SEP-2004.

PD

XX 27-FEB-2004; 2004WO-JP002438.

PF

XX 28-FEB-2003; 2003JP-00052926.

PR

XX (KISO/) KISO Y.

PA

XX Kiso Y;

PI

XX WPI; 2004-661989/64.

DR

XX Novel compound such as beta-secretase inhibitor, useful as preventive or

PT therapeutic agent for treating neurodegenerative disease such as

PT Alzheimer's disease, Parkinson's disease and neuropathy.

XX

XX Example 36; SEQ ID NO 35; 143pp; Japanese.

PS

XX The invention comprises beta-secretase inhibitory peptides. The beta-

CC secretase inhibitory peptides of the invention are useful for the

CC prevention or treatment of neurodegenerative diseases, such as:

CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,

CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides

CC of the invention are also useful in the manufacture of an APPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 8; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 1 VLXDAEF 7

RESULT 13
 AAY94771
 ID AAY94771 standard; protein; 8 AA.

XX AC

XX AAY94771;

DT 12-FEB-2001 (first entry)

DE Beta-secretase substrate peptide SEQ ID 17.

XX Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;

KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.

XX OS Synthetic.

XX PN WO200058479-A1.

XX PD 05-OCT-2000.

XX PF 23-MAR-2000; 2000WO-US007755.

XX PR 26-MAR-1999; 99US-00277229.

XX PA (AMGE-) AMGEN INC.

XX PI Citron M, Vassar RJ, Bennett BD;

XX DR WPI; 2000-594643/56.

XX Isolated beta-secretase nucleic acids and encoded polypeptides, useful
 XX for diagnosis and gene therapy of Alzheimer's disease.

XX Example 10; Page 117; 145pp; English.

XX This invention relates to 3 nucleotide sequences encoding beta-secretase
 CC proteins. Beta-secretase is an enzyme involved in the production of one
 CC of the components of amyloid plaques involved in Alzheimer's disease. The
 CC invention includes an expression vector comprising the nucleotide
 CC sequence, a host cell comprising the expression vector, and a process for
 CC producing the protein through culturing the transformed cells. Also
 CC included in the invention are a polypeptide derivative of the beta-
 CC secretase protein, a fusion protein comprising beta-secretase fused to a
 CC heterologous amino acid sequence, and a method for modulating the levels
 CC of beta-secretase polypeptide in a mammal comprising administering the
 CC polynucleotide sequence. Beta-secretase exhibits neuroprotective and
 CC neurotropic activity. The beta-secretase nucleotide sequence may be used to
 CC map locations of the beta-secretase gene and related genes on chromosomes
 CC and as hybridization probes in diagnostic assays to test for the presence
 CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
 CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
 CC used as anti-sense inhibitors of beta-secretase expression, in gene
 CC therapy of Alzheimer's disease, and for the identification of compounds
 CC that modulate beta-secretase activity. Antibodies to the beta-secretase
 CC protein may be used for in vitro and in vivo diagnostic purposes to
 CC detect the presence of beta-secretase polypeptide in a body fluid or cell
 CC sample. The present sequence represents a beta-secretase substrate
 XX peptide

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 3; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 2 VNLDAEF 8

RESULT 14
 AAY94772

ID AAY94772 standard; protein; 8 AA.

XX AC AAY94772;

XX DT 12-FEB-2001 (first entry)

XX DE Beta-secretase substrate peptide SEQ ID 18.

XX KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;

XX Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.

XX OS Synthetic.

XX PN WO200058479-A1.

XX PD 05-OCT-2000.

XX PF 23-MAR-2000; 2000WO-US007755.

XX PR 26-MAR-1999; 99US-00277229.

XX PA (AMGE-) AMGEN INC.

XX PI Citron M, Vassar RJ, Bennett BD;

XX DR WPI; 2000-594643/56.

XX Isolated beta-secretase nucleic acids and encoded polypeptides, useful
 XX for diagnosis and gene therapy of Alzheimer's disease.

XX Example 10; Page 117; 145pp; English.

XX This invention relates to 3 nucleotide sequences encoding beta-secretase
 CC proteins. Beta-secretase is an enzyme involved in the production of one
 CC of the components of amyloid plaques involved in Alzheimer's disease. The
 CC invention includes an expression vector comprising the nucleotide
 CC sequence, a host cell comprising the expression vector, and a process for
 CC producing the protein through culturing the transformed cells. Also
 CC included in the invention are a polypeptide derivative of the beta-
 CC secretase protein, a fusion protein comprising beta-secretase fused to a
 CC heterologous amino acid sequence, and a method for modulating the levels
 CC of beta-secretase polypeptide in a mammal comprising administering the
 CC polynucleotide sequence. Beta-secretase exhibits neuroprotective and
 CC neurotropic activity. The beta-secretase nucleotide sequence may be used to
 CC map locations of the beta-secretase gene and related genes on chromosomes
 CC and as hybridization probes in diagnostic assays to test for the presence
 CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
 CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
 CC used as anti-sense inhibitors of beta-secretase expression, in gene
 CC therapy of Alzheimer's disease, and for the identification of compounds
 CC that modulate beta-secretase activity. Antibodies to the beta-secretase
 CC protein may be used for in vitro and in vivo diagnostic purposes to
 CC detect the presence of beta-secretase polypeptide in a body fluid or cell
 CC sample. The present sequence represents a beta-secretase substrate
 XX peptide

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 3; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|

Db 2 VKMDAEF 8

RESULT 15
AAY94773
ID AAY94773 standard; protein; 8 AA.
XX
AC
XX
AC AAY94773;
XX
DT 12-FEB-2001 (first entry)
XX
DE
XX
KW Beta-secretase substrate peptide SEQ ID 19.
KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;
KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
XX
OS Synthetic.
XX
PN WO200058479-A1.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US007755.
XX
PR 26-MAR-1999; 99US-00277229.
XX
PA (AMGE-) AMGEN INC.
XX
PI Citron M, Vassar RJ, Bennett BD;
XX
DR WPI; 2000-594643/56.
XX
XX Isolated beta-secretase nucleic acids and encoded polypeptides, useful
PT for diagnosis and gene therapy of Alzheimer's disease.
XX
PS Example 10; Page 117; 145pp; English.
XX
CC This invention relates to 3 nucleotide sequences encoding beta-secretase
CC proteins. Beta-secretase is an enzyme involved in the production of one
CC of the components of amyloid plaques involved in Alzheimer's disease. The
CC invention includes an expression vector comprising the nucleotide
CC sequence, a host cell comprising the expression vector, and a process for
CC producing the protein through culturing the transformed cells. Also
CC included in the invention are a polypeptide derivative of the beta-
CC secretase protein, a fusion protein comprising beta-secretase fused to a
CC heterologous amino acid sequence, and a method for modulating the levels
CC of beta-secretase polypeptide in a mammal comprising administering the
CC polynucleotide sequence. Beta-secretase exhibits neuroprotective and
CC neurotropic activity. The beta-secretase nucleotide sequence may be used to
CC map locations of the beta-secretase gene and related genes on chromosomes
CC and as hybridization probes in diagnostic assays to test for the presence
CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's
CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be
CC used as anti-sense inhibitors of beta-secretase expression, in gene
CC therapy of Alzheimer's disease, and for the identification of compounds
CC that modulate beta-secretase activity. Antibodies to the beta-secretase
CC protein may be used for in vitro and in vivo diagnostic purposes to
CC detect the presence of beta-secretase polypeptide in a body fluid or cell
CC sample. The present sequence represents a beta-secretase substrate
CC peptide
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|

Db 2 VKMDAEF 8

RESULT 17
AAU07230
ID AAU07230 standard; peptide; 8 AA.
XX
AC AAU07230;
XX

Db 2 VKDAEF 8

RESULT 16
AAB07872
ID AAB07872 standard; peptide; 8 AA.
XX
AC AAB07872;
XX
DT 14-NOV-2000 (first entry)
XX
DE A beta-secretase inhibitor peptide.
XX
KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "hydroxyethylene"
XX
PN WO200047618-A2.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000WO-US003819.
XX
PR 10-FEB-1999; 99US-0119571P.
PR 15-JUN-1999; 99US-0139172P.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
XX
DR WPI; 2000-533011/48.
XX
PT Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
XX Alzheimer's disease.
XX
PS Disclosure; Page 12; 121pp; English.
XX
CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents an inhibitor of beta-secretase enzyme
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|

Db 2 VMXVAEF 8

RESULT 17
AAU07230
ID AAU07230 standard; peptide; 8 AA.
XX
AC AAU07230;
XX

DT 24-OCT-2001 (first entry)
 XX Human beta-amyloid protein precursor, APP-beta secretase site peptide #3.
 DE
 XX
 XX Human, aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease; APP-beta.
 XX
 XX Homo sapiens.
 XX WO200149097-A2.
 PN
 XX
 XX 12-JUL-2001.
 PD
 XX
 XX 09-MAY-2001; 2001WO-IB000797.
 PF
 XX
 XX 09-MAY-2001; 2001WO-IB000797.
 PR
 XX
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 PI WPI; 2001-502548/55.
 DR
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 PT
 XX
 XX Claim 88; Page 94; 185pp; English.
 PS
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing an
 CC APP cleavage site recognisable by a mammalian beta-secretase, and further
 CC comprising two lysine residues at the carboxyl terminus of the amino acid
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used
 CC for assaying for modulators of beta-secretase activity; identifying
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl
 CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
 CC Agents identified by the above methods are useful for treating
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta
 CC (Abeta) peptide production, for use in designing therapeutics for the
 CC treatment or prevention of Alzheimer's disease. Probes and primers
 CC derived from APP nucleic acid sequences are useful for detecting Hu-Asp
 CC nucleic acids in vitro assays and in Northern and Southern blots. The
 CC present sequence represents the amino acid sequence of human amyloid
 CC protein precursor, APP-beta secretase site peptide substrate #3 used in
 CC assays of human Asp2 beta- secretase activity
 CC
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXXAEF 7
 |:::|
 Db 2 VKMDAEF 8
 RESULT 18
 AAEL0661
 ID AAE10661 standard; peptide; 8 AA.
 XX

AC AAE10661;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human aspartyl protease-1 beta-secretase Swedish mutant peptide.
 XX
 KW Human; aspartyl protease 1; Aspi; amyloid precursor protein; APP;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
 KW aspartyl protease-1 beta-secretase Swedish mutant peptide.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 4..5
 FT
 XX GB2357767-A.
 PN
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA
 XX Bienkowski MJ, Gurney M;
 PI WPI; 2001-444208/48.
 XX
 DR
 XX Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Example 15; Page 92; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Aspi) or modified Aspi
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Aspi alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Aspi alpha-secretase
 CC activity, where modulators that increase hu-Aspi alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Aspi protease substrate is useful
 CC for assaying hu-Aspi proteolytic activity, by contacting hu-Aspi protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Aspi proteolytic activity. The present sequence is human aspartyl
 CC protease-1 (hu-Asp-1) beta-secretase Swedish (Sw) mutant peptide which is
 CC used for determining the enzymatic activity of Asp-1 protein lacking a
 CC transmembrane (TM) domain and containing (His)6 tag
 CC
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXXAEF 7
 |:::|
 Db 2 VNLDAEF 8
 RESULT 19
 AAEL0660
 ID AAE10660 standard; peptide; 8 AA.
 XX

AC AAE10660;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human Aspartyl protease-1 (hu-Asp-1) beta-secretase, wild-type peptide.
 XX
 KW Human; aspartyl protease 1; Aspl1; amyloid precursor protein; APP;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 4. .5
 XX
 PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 XX 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Example 15; Page 92; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is human aspartyl
 CC protease-1 (hu-Asp-1) beta-secretase, wild-type peptide which is used for
 CC determining the enzymatic activity of Asp-1 protein lacking a
 CC transmembrane (TM) domain and containing (His)6 tag
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 |:::|
 Db 2 VKMDAEF 8
 RESULT 20
 AAE06902
 ID AAE06902 standard; peptide; 8 AA.
 XX
 AC AAE06902;
 XX

DT 23-OCT-2001 (first entry)
 XX
 DE Human amyloid precursor protein (APP) substrate peptide.
 XX
 KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nontropic;
 KW neuroprotective; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200150829-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB000799.
 XX
 PR 09-MAY-2001; 2001WO-IB000799.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-483072/52.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 XX
 PS Claim 128; Page 101; 185pp; English.
 XX
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.
 CC Human aspartyl proteases can act as beta-secretase proteases useful for
 CC treating Alzheimer's disease. APP isoforms are useful for identifying
 CC modulators of amyloid-beta peptide production, for use in designing
 CC therapeutics for the treatment and prevention of Alzheimer's disease,
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
 CC and neuronal loss. APP isoforms are also used in methods for identifying
 CC inhibitors and modulators of human Asp2 activity. The invention relates
 CC to a method for identifying agents that modulate the activity of human
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 CC as a means to screen in cellular assays for the inhibitors of beta- and
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
 CC The present sequence is human amyloid precursor protein (APP) substrate
 CC peptide related to the invention
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 |:::|
 Db 2 VKMDAEF 8
 RESULT 21
 AAB61348
 ID AAB61348 standard; peptide; 8 AA.
 XX
 AC AAB61348;
 XX
 DT 02-APR-2001 (first entry)
 XX

```

DE Peptide OM99-2.
KW Memapsin 2; catalyst; Alzheimer's.
XX
OS Unidentified.
XX
PN WO200100663-A2.
XX
PD 04-JAN-2001.
XX
XX 27-JUN-2000; 2000WO-US017661.
PF
XX 28-JUN-1999; 99US-0141363P.
PR
PR 30-NOV-1999; 99US-0168060P.
PR 25-JAN-2000; 2000US-0177836P.
PR 27-JAN-2000; 2000US-0178368P.
PR 08-JUN-2000; 2000US-0210292P.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JJN, Lin X, Koelsch G;
PI
XX WPI; 2001-102885/11.
DR
XX Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease.
XX
XX Example 7; Page 36; 86pp; English.
PS
XX The present invention relates to a purified recombinant catalytically
CC active memapsin 2. The invention may be used for isolating inhibitors
CC which are used to treat or prevent Alzheimer's disease. The invention may
CC also be used to screen for individuals more genetically prone to develop
CC Alzheimer's disease
XX
XX Sequence 8 AA;
SQ
    Query Match      100.0%; Score 7; DB 4; Length 8;
    Best Local Similarity 57.1%; Pred. No. 1.8e+06;
    Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VNLAEEF 8
    |::|||
    |::|||

RESULT 22
AAE02613
ID AAE02613 standard; peptide; 8 AA.
XX
AC AAE02613;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human Aspartyl protease-1 beta-secretase Swedish mutant form peptide.
XX
XX Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
XX beta-secretase.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Cleavage-site 4..5
FT
XX WO200123533-A2.
XX
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US026080.
PF
XX 23-SEP-1999; 99US-0155493P.
PR
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
PA
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.

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PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
PA
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
XX Example 15; Page 94; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
CC (hu-Asp-1) beta-secretase, Swedish (Sw) mutant form peptide which is used
CC for determining the enzymatic activity of Asp-1 deltaTM (His)6 protein
XX
XX Sequence 8 AA;
SQ
    Query Match      100.0%; Score 7; DB 4; Length 8;
    Best Local Similarity 57.1%; Pred. No. 1.8e+06;
    Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VNLAEEF 8
    |::|||
    |::|||

RESULT 23
AAE02612
ID AAE02612 standard; peptide; 8 AA.
XX
AC AAE02612;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human Aspartyl protease-1 (hu-Asp-1) beta-secretase, wild-type peptide.
XX
XX Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
XX beta-secretase.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Cleavage-site 4..5
FT
XX WO200123533-A2.
XX
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US026080.
PF
XX 23-SEP-1999; 99US-0155493P.
PR
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
PA
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.

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XX PS Example 15; Page 94; 189pp; English.
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
XX CC (hu-Asp-1) beta-secretase, wild-type peptide which is used for
XX CC determining the enzymatic activity of Asp-1 deltaTM (His)6 protein
XX CC
XX CC Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 2 VNMDAEF 8
RESULT 24
AAB66586
ID AAB66586 standard; peptide; 8 AA.
XX AC AAB66586;
XX KW Human memapsin 2 inhibitor OM99-2.
XX DT 12-APR-2001 (first entry)
XX DE Human memapsin 2 inhibitor OM99-2.
XX
XX KW Human memapsin 2; neurotropic; neuroprotective; amyloid precursor protein;
XX KW APP; memapsin 2 inhibitor; Alzheimer's disease.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4..5
XX FT /note= "residues 4 and 5 form a Leu-Ala dipeptide
XX FT isostere"
XX
XX PN WO200100665-A2.
XX
XX PD 04-JAN-2001.
XX
XX PF 27-JUN-2000; 2000WO-US017742.
XX
XX PR 28-JUN-1999; 99US-0141363P.
XX PR 30-NOV-1999; 99US-0168060P.
XX PR 25-JAN-2000; 2000US-0177836P.
XX PR 27-JAN-2000; 2000US-0178368P.
XX PR 08-JUN-2000; 2000US-0210292P.
XX
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PA (UNII ) UNIV ILLINOIS FOUND.
XX
XX PI Tang JJN, Hong L, Ghosh AK;
XX
XX DR WPI; 2001-137933/14.
XX
XX PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
XX PT having 2 catalytic aspartic residues and substrate binding cleft, used to
XX PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.
XX
XX PS Example 7; Page 36; 86pp; English.
XX CC The present sequence is given in a specification relating to an inhibitor
XX CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
XX CC active site, which is defined by the presence of two catalytic aspartic
XX CC residues and a substrate binding cleft. The inhibitor is useful for the
XX CC treatment and diagnosis of Alzheimer's disease. It is useful in screens

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CC for individuals with a genetic predisposition to Alzheimer's disease. The
CC inhibitor is useful as a reagent for specifically binding to memapsin 2
CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,
CC purification and characterisation
XX CC
XX CC Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 2 VNLAEEF 8
RESULT 25
AAB97467
ID AAB97467 standard; protein; 8 AA.
XX AC AAB97467;
XX DT 03-AUG-2001 (first entry)
XX DE Asp2 inhibitory peptide OM99-2.
XX
XX KW Asp2; endorepsin 2; memapsin 2; beta-amyloid protein;
XX KW Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;
XX KW Asp2 inhibitor.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 4..5
XX FT /note= "designated hydroxyethylene transition state
XX FT isostere"
XX
XX PN WO200129563-A1.
XX
XX PD 26-APR-2001.
XX
XX PF 19-OCT-2000; 2000WO-GB004039.
XX
XX PR 21-OCT-1999; 99GB-00024957.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Christie G, Hussain I, Powell DJ;
XX
XX DR WPI; 2001-300381/31.
XX
XX PT Screening for inhibitors of Asp 2 mediated polypeptide cleavage comprises
XX PT measuring substrate cleavage or ligand binding with a system comprising
XX PT Asp 2 and a substrate or labelled ligand in the presence or absence of a
XX PT test compound.
XX
XX PS Disclosure; Page 2; 34pp; English.
XX
XX CC The present invention describes a method of screening for compounds which
XX CC inhibit Asp2 (also known as memapsin 2 and endorepsin 2) mediated
XX CC cleavage of a protein substrate, involving measuring the extent of
XX CC cleavage of the substrate in the presence and absence of the test
XX CC compound. Asp2 is thought to be involved in the cleavage of amyloid
XX CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid
XX CC is involved in the pathogenesis of Alzheimer's disease. Parkinson's
XX CC disease, cortical Lewy body disease and vascular and cerebrovascular
XX CC diseases, and Asp2 inhibitors could be useful in their treatment. The
XX CC present sequence is an inhibitor of Asp2
XX CC
XX CC Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 4; Length 8;

```

Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 26
AAU06635
ID AAU06635 standard; peptide; 8 AA.
AC AAU06635;
XX
DT 24-OCT-2001 (first entry)
XX
DE Synthetic fluorescent Asp2 substrate.
XX
KW Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;
KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Glu is covalently linked to a fluorescent MCA moiety"
FT Modified-site 8
FT Modified-site 8 /note= "Glu is covalently linked to a fluorescent K-DNP moiety"
FT
XX
XX WO200149098-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB000798.
XX
XX 09-MAY-2001; 2001WO-IB000798.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-502549/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Example 12; Page 81; 185pp; English.
XX
XX The invention relates to a purified polypeptide comprising a fragment of
XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
XX transmembrane domain and the Asp2 protein, and where the polypeptide and
XX the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. The invention also details polynucleotides for the Asp proteins
XX and vectors expressing them, and a polypeptide (isoform of amyloid
XX protein precursor (APP)) comprising the amino acid sequence of an APP or
XX its fragment containing an APP cleavage site recognizable by a mammalian
XX beta-secretase, and further comprising two lysine residues at the
XX carboxyl terminus of the amino acid sequence of the mammalian APP or APP
XX fragment. Also included in the invention are methods of identifying
XX modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
XX useful for treating Alzheimer's disease. APP is useful in methods for
XX identifying inhibitors or modulators of human Asp2 activity and amyloid-
XX beta (Abeta) peptide production. APP is also useful in designing
XX therapeutics for the treatment or prevention of Alzheimer's disease. APP
XX comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is

CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridize to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC Southern blots. The present sequence is a synthetic fluorescent substrate
CC used to assay Asp2
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 27
AAU06631
ID AAU06631 standard; peptide; 8 AA.
XX
AC AAU06631;
XX
DT 24-OCT-2001 (first entry)
XX
DE Beta secretase substrate peptide.
XX
KW Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;
KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta;
KW Beta secretase substrate peptide.
XX
XX Synthetic.
XX
XX WO200149098-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB000798.
XX
XX 09-MAY-2001; 2001WO-IB000798.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-502549/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Claim 88; Page 94; 185pp; English.
XX
XX The invention relates to a purified polypeptide comprising a fragment of
XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
XX transmembrane domain and the Asp2 protein, and where the polypeptide and
XX the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. The invention also details polynucleotides for the Asp proteins
XX and vectors expressing them, and a polypeptide (isoform of amyloid
XX protein precursor (APP)) comprising the amino acid sequence of an APP or
XX its fragment containing an APP cleavage site recognizable by a mammalian
XX beta-secretase, and further comprising two lysine residues at the
XX carboxyl terminus of the amino acid sequence of the mammalian APP or APP
XX fragment. Also included in the invention are methods of identifying
XX modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
XX useful for treating Alzheimer's disease. APP is useful in methods for

CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
 CC associated with increased levels of Abeta processing is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridize to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is a Beta secretase substrate
 CC peptide
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 2 VKMDAEF 8

RESULT 28

ABG78391
 ID ABG78391 standard; peptide; 8 AA.

XX AC ABG78391;

DT 15-NOV-2002 (first entry)

XX DE Memapsin 2 inhibitor OM99-2.

XX KW Memapsin 2; aspartic protease; beta secretase; inhibitor;
 KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
 KW APP; neuroprotective; nontropic; substrate side-chain preference.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200253594-A2.

XX PD 11-JUL-2002.

XX PF 28-DEC-2001; 2001WO-US050826.

XX PR 28-DEC-2000; 2000US-0258705P.

XX PR 14-MAR-2001; 2001US-0275756P.

XX XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.

XX PI Tang JJN, Koelsch G, Ghosh AK;

XX DR WPI; 2002-619088/66.

XX XX New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
 PT disease.

XX PS Example 3; Page 32; 74pp; English.

XX CC The invention relates to an inhibitor of catalytically active memapsin 2
 CC (an aspartic protease which can cleave at beta secretase sites), which
 CC binds to the active site of memapsin 2 defined by the presence of two
 CC catalytic aspartic residues and substrate binding cleft. Also included is
 CC a method of determination of the substrate side-chain preference in
 CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
 CC substrates with memapsin 2, and determining the sub-site preference of
 CC memapsin 2 by determining relative initial hydrolysis rates of the
 CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
 CC library of memapsin 2 inhibitors containing a base sequence taken from
 CC OM99-2 (Glu-Val-Asn-Leu-Ala-Glu-phe), probing the library of
 CC inhibitors with memapsin 2 which binds to several inhibitors to generate

CC several bound memapsin 2, and detecting the bound memapsin 2 with an
 CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
 CC secondary antibody. The inhibitors may be used in the manufacture of a
 CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
 CC be involved in the cleavage of amyloid precursor protein (APP), and for
 CC determining the substrate side-chain preference in memapsin 2 sub-sites.
 CC The present sequence represents a potential or actual inhibitor of human
 CC memapsin 2
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 2 VNLADEF 8

RESULT 29

ABG78392

ID ABG78392 standard; peptide; 8 AA.

XX AC ABG78392;

XX DT 15-NOV-2002 (first entry)

XX DE Memapsin 2 substrate cleavage site template #1.

XX KW Human; memapsin 2; aspartic protease; beta secretase;
 KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
 KW APP; neuroprotective; nontropic; inhibitor; subsite template;
 KW substrate side-chain preference.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200253594-A2.

XX PD 11-JUL-2002.

XX PF 28-DEC-2001; 2001WO-US050826.

XX PR 28-DEC-2000; 2000US-0258705P.

XX PR 14-MAR-2001; 2001US-0275756P.

XX XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNII) UNIV ILLINOIS FOUND.

XX PI Tang JJN, Koelsch G, Ghosh AK;

XX DR WPI; 2002-619088/66.

XX XX New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
 PT disease.

XX PS Example 5; Page 49; 74pp; English.

XX CC The invention relates to an inhibitor of catalytically active memapsin 2
 CC (an aspartic protease which can cleave at beta secretase sites), which
 CC binds to the active site of memapsin 2 defined by the presence of two
 CC catalytic aspartic residues and substrate binding cleft. Also included is
 CC a method of determination of the substrate side-chain preference in
 CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
 CC substrates with memapsin 2, and determining the sub-site preference of
 CC memapsin 2 by determining relative initial hydrolysis rates of the
 CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
 CC library of memapsin 2 inhibitors containing a base sequence taken from
 CC OM99-2 (Glu-Val-Asn-Leu-Ala-Glu-phe), probing the library of
 CC inhibitors with memapsin 2 which binds to several inhibitors to generate
 CC several bound memapsin 2, and detecting the bound memapsin 2 with an
 CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated

CC secondary antibody. The inhibitors may be used in the manufacture of a
 CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
 CC be involved in the cleavage of amyloid precursor protein (APP), and for
 CC determining the substrate side-chain preference in memapsin 2 sub-sites.
 CC The present sequence represents a subsite template peptide used to
 CC determine the substrate specificity of human memapsin 2
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 2 VNLADEF 8
 RESULT 30
 ABG78439
 ID ABG78439 standard; peptide; 8 AA.
 AC ABG78439;
 XX
 DT 15-NOV-2002 (first entry)
 DE Memapsin inhibitor library base sequence.
 XX
 KW Memapsin 2; aspartic protease; beta secretase; inhibitor;
 KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
 KW APP; neuroprotective; nootropic; substrate side-chain preference.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200253594-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 28-DEC-2001; 2001WO-US050826.
 XX
 PR 28-DEC-2000; 2000US-0258705P.
 PR 14-MAR-2001; 2001US-0275756P.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Tang JJN, Koelsch G, Ghosh AK;
 XX
 DR WPI; 2002-619088/66.
 XX
 PT New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
 PT disease.
 XX
 PS Example 5; Page 56; 74pp; English.
 XX
 CC The invention relates to an inhibitor of catalytically active memapsin 2
 CC (an aspartic protease which can cleave at beta secretase sites), which
 CC binds to the active site of memapsin 2 defined by the presence of two
 CC catalytic aspartic residues and substrate binding cleft. Also included is
 CC a method of determination of the substrate side-chain preference in
 CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
 CC substrates with memapsin 2, and determining the sub-site preference of
 CC memapsin 2 by determining relative initial hydrolysis rates of the
 CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
 CC library of memapsin 2 inhibitors containing a base sequence taken from
 CC OM99-2 (Glu-Val-Asn-Leu-Ala-Glu-phe), probing the library of
 CC inhibitors with memapsin 2 which binds to several inhibitors to generate
 CC several bound memapsin 2, and detecting the bound memapsin 2 with an
 CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
 CC secondary antibody. The inhibitors may be used in the manufacture of a
 CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
 CC be involved in the cleavage of amyloid precursor protein (APP), and for

CC determining the substrate side-chain preference in memapsin 2 sub-sites.
 CC The present sequence represents a potential or actual inhibitor of human
 CC memapsin 2
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 2 VNLADEF 8
 RESULT 31
 ABB78621
 ID ABB78621 standard; peptide; 8 AA.
 XX
 AC ABB78621;
 XX
 DT 16-JUL-2002 (first entry)
 DE APP Swedish mutant form beta-secretase processing site SEQ ID NO:70.
 XX
 KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
 XX
 OS Synthetic.
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-00025934.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 PR 22-SEP-2000; 2000GB-00023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2002-397167/43.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
 XX
 PS Example 12; Page 85; 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the non
 CC coding strand complementary to a defined 1804 nucleotide sequence (see
 CC ABL2456) where the nucleotide sequence encodes a polypeptide having Asp1
 CC proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as

CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents the amino acid sequence of a peptide that includes
 CC the beta-secretase processing site within the Swedish mutant form of
 CC amyloid precursor protein (APP), which is used in an example from the
 CC present invention
 CC
 XX Sequence 8 AA;

Query Match 100.0%; Score 7; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 |:::|
 Db 2 VKMDAEF 8

RESULT 32
 ABB78622
 ID ABB78622 standard; peptide; 8 AA.
 XX AC ABB78622;
 XX DT 16-JUL-2002 (first entry)
 XX Human beta secretase peptide SEQ ID NO:71.
 DE Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
 KW Homo sapiens.
 OS
 XX GB2367060-A.
 XX 27-MAR-2002.
 XX 29-OCT-2001; 2001GB-00025934.
 XX 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 13-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 PR 22-SEP-2000; 2000GB-00023315.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Bienkowski MJ, Gurney M;
 XX WPI; 2002-397167/43.
 XX Human aspartyl protease 1 substrates useful in assays to detect aspartyl
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
 XX Example 15; Page 92; 182pp; English.

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (i) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the non
 CC -coding strand complementary to a defined 1804 nucleotide sequence (see
 CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
 CC proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease

CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents a human beta secretase peptide, which is used in an
 CC example from the present invention
 XX Sequence 8 AA;

Query Match 100.0%; Score 7; DB 5; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 |:::|
 Db 2 VNLDAEF 8

RESULT 33
 AAU99503
 ID AAU99503 standard; peptide; 8 AA.
 XX AC AAU99503;
 XX DT 07-OCT-2002 (first entry)
 XX Human memapsin 2 inhibitor, OM99-2.
 DE Human; memapsin 2; beta secretase; aspartic protease; APP;
 KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
 KW neuroprotective; nootropic.
 XX Synthetic.
 XX US2002049303-A1.
 XX 25-APR-2002.
 XX 28-FEB-2001; 2001US-00796264.
 XX 28-JUN-1999; 99US-0141363P.
 PR 30-NOV-1999; 99US-0168060P.
 PR 25-JAN-2000; 2000US-0177836P.
 PR 27-JAN-2000; 2000US-0178368P.
 PR 27-JUN-2000; 2000US-00604608.
 XX (TANG/) TANG J J N.
 PA (LINK/) LIN X.
 PA (KOEL/) KOELSCH G.
 PA (HONG/) HONG L.
 XX Tang JJN, Lin X, Koelsch G, Hong L;
 XX WPI; 2002-507280/54.
 XX New recombinant catalytically active memapsin 2, useful to screen for
 PT inhibitors of memapsin 2 which can be used to prevent and treat
 PT Alzheimer's disease.
 XX Example 7; Page 13; 44pp; English.

CC The present invention relates to methods for the production of purified,
 CC recombinant catalytically active, memapsin 2 (beta secretase). Memapsin
 CC 2, a member of the aspartic protease family, cleaves beta-amyloid
 CC precursor protein (APP) found in amyloid plaques. The recombinant
 CC memapsin 2 is useful for identifying inhibitors of memapsin 2 in the
 CC design of drugs for the treatment and/or prevention of Alzheimer's
 CC disease. The recombinant memapsin 2 can be used to immunise against
 CC Alzheimer's disease. The present sequence represents a synthetic
 CC inhibitor of human memapsin 2
 XX Sequence 8 AA;


```

Query Match      100.0%; Score 7; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
DB 2 VNLAAEF 8

RESULT 34
ID ABG76115 standard; peptide; 8 AA.
AC ABG76115;
XX
XX 01-MAY-2003 (first entry)
XX
XX Synthetic memapsin 2 inhibitor OM99-2.
XX
XX Memapsin 2; beta-secretase; beta-amyloid precursor protein;
XX beta-amyloid peptide; Alzheimer's disease; neurotropic; neuroprotective;
XX substrate analogue; inhibitor; OM99-2.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 4..5
XX /label= OTHER
XX /note= "The bond between these two residues is a
XX transition-state analogue isostere (-CH(OH)-CH2-)"
XX
XX US2002164760-A1.
XX
XX 07-NOV-2002.
XX
XX 28-FEB-2001; 2001US-00795903.
XX
XX 28-JUN-1999; 99US-0141363P.
XX 30-NOV-1999; 99US-0168060P.
XX 25-JAN-2000; 2000US-0177836P.
XX 27-JAN-2000; 2000US-0178368P.
XX 08-JUN-2000; 2000US-0210292P.
XX 27-JUN-2000; 2000US-00604608.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Lin X, Koelach G, Tang JJN;
XX WPI; 2003-255218/25.
XX
XX New purified recombinant catalytically active memapsin 2 (beta-
XX secretase), useful for designing and screening of specific inhibitors for
XX the diagnosis, prevention and/or treatment of Alzheimer's disease.
XX
XX Example 7; Page 12; 44pp; English.
XX
XX The invention relates to a purified recombinant catalytically active
XX memapsin 2, a beta-secretase which produces the beta-amyloid peptide from
XX the beta amyloid precursor protein. Also included are producing the above
XX memapsin 2 (comprising refolding the recombinant memapsin 2 under
XX conditions which dissociate and then slowly refold the enzyme into a
XX catalytically active form), isolating inhibitors of cleavage by memapsin
XX 2 (comprising adding to one or more potential inhibitors the memapsin 2
XX and a substrate for memapsin 2 and screening for decreased cleavage of
XX the substrate by the inhibitors), designing or obtaining inhibitors of
XX the memapsin 2 (comprising modelling an inhibitor based on the
XX crystallisation coordinates of memapsin 2 or the parameters given in the
XX specification), a database comprising binding properties and chemical
XX structures of compounds designed or screened by the method above and
XX treating or preventing Alzheimer's disease (comprising administering to a
XX patient an inhibitor of memapsin 2 which binds to the active site of the
XX memapsin 2 defined by the presence of 2 catalytic aspartic residues and

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substrate binding cleft or immunising an individual with the above
memapsin 2 to elicit an amount of antibodies to reduce the cleavage by
endogenous memapsin 2). The memapsin 2 is useful in designing and
screening of specific inhibitors for the diagnosis, prevention and/or
treatment of Alzheimer's disease. The present sequence represents a
synthetic substrate analogue and inhibitor of memapsin 2
XX
XX Sequence 8 AA;
Query Match      100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
DB 2 VNLAAEF 8

RESULT 35
ID ABR54160 standard; peptide; 8 AA.
AC ABR54160;
XX
XX 19-JUN-2003 (first entry)
XX
XX Beta-secretase substrate peptide #258.
XX
XX Beta-secretase; neurotropic; neuroprotective; Secretase Inhibitor Beta;
XX substrate; beta-APP; amyloid precursor protein; Alzheimer's disease;
XX amyloid beta peptide deposition; Down's syndrome.
XX
XX Synthetic.
XX
XX WO200294985-A2.
XX
XX 28-NOV-2002.
XX
XX 17-MAY-2002; 2002WO-US015590.
XX
XX 22-MAY-2001; 2001US-0292591P.
XX 30-AUG-2001; 2001US-0316115P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bruce JE, Tang X, Garsky V, Brady SF, Li Y, Chen-Dodson E;
XX Sardana M, Shafer JA;
XX WPI; 2003-148462/14.
XX
XX New beta-secretase substrate peptides, useful as substrates in assays for
XX measuring beta-secretase activity, or for screening test compounds for
XX the ability to inhibit beta-secretase activity used for treating
XX Alzheimer's disease.
XX
XX Claim 1; Page 34; 103pp; English.
XX
XX The invention relates to a novel substantially pure beta-secretase
XX substrate peptide. A peptide of the invention has neurotropic, and
XX neuroprotective activity. The peptide acts as a Secretase Inhibitor Beta.
XX The beta-secretase substrate peptides are useful as substrates in various
XX assays for measuring beta-secretase activity. The methods are useful for
XX screening test compounds for the ability to inhibit beta-secretase
XX activity, or inhibiting the cleavage of beta-APP (amyloid precursor
XX protein) in mammalian hosts, which can be used for treating conditions
XX related to amyloid beta peptide deposition, e.g. Alzheimer's disease or
XX Down's syndrome. The present sequence represents a beta secretase
XX substrate peptide of the invention
XX
XX Sequence 8 AA;
Query Match      100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;

```

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 2 VNLAAEF 8

RESULT 36

ABR54161
ID ABR54161 standard; peptide; 8 AA.

XX AC ABR54161;
XX DT 19-JUN-2003 (first entry)

XX XX Beta-secretase substrate peptide #259.

XX KW Beta-secretase; neurotrophic; neuroprotective; Secretase Inhibitor Beta;
KW substrate; beta-APP; amyloid precursor protein; Alzheimer's disease;
KW amyloid beta peptide deposition; Down's syndrome.

XX OS Synthetic.

XX PN WO200294985-A2.

XX XX 28-NOV-2002.

XX PF 17-MAY-2002; 2002WO-US015590.

XX PR 22-MAY-2001; 2001US-0292591P.

XX PR 30-AUG-2001; 2001US-0316115P.

XX XX (MERI) MERCK & CO INC.

XX PI Bruce JE, Tang X, Garsky V, Brady SF, Li Y, Chen-Dodson E;
PI Sardana M, Shafer JA;

XX DR WPI; 2003-148462/14.

XX PT New beta-secretase substrate peptides, useful as substrates in assays for
PT measuring beta-secretase activity, or for screening test compounds for
PT the ability to inhibit beta-secretase activity used for treating
PT Alzheimer's disease.

XX PS Claim 1; Fig 6; 103pp; English.

XX CC The invention relates to a novel substantially pure beta-secretase
CC substrate peptide. A peptide of the invention has neurotrophic, and
CC neuroprotective activity. The peptide acts as a Secretase Inhibitor Beta.
CC The beta-secretase substrate peptides are useful as substrates in various
CC assays for measuring beta-secretase activity. The methods are useful for
CC screening test compounds for the ability to inhibit beta-secretase
CC activity, or inhibiting the cleavage of beta-APP (amyloid precursor
CC protein) in mammalian hosts, which can be used for treating conditions
CC related to amyloid beta peptide deposition, e.g. Alzheimer's disease or
CC Down's syndrome. The present sequence represents a beta secretase
CC substrate peptide of the invention

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 2 VNFPAEF 8

RESULT 37

ABR54159
ID ABR54159 standard; peptide; 8 AA.

XX

AC

XX ABR54159;

XX DT 19-JUN-2003 (first entry)

XX DE Beta-secretase substrate peptide #257.

XX KW Beta-secretase; neurotrophic; neuroprotective; Secretase Inhibitor Beta;
KW substrate; beta-APP; amyloid precursor protein; Alzheimer's disease;
KW amyloid beta peptide deposition; Down's syndrome.

XX OS Synthetic.

XX PN WO200294985-A2.

XX XX 28-NOV-2002.

XX PF 17-MAY-2002; 2002WO-US015590.

XX PR 22-MAY-2001; 2001US-0292591P.

XX PR 30-AUG-2001; 2001US-0316115P.

XX PA (MERI) MERCK & CO INC.

XX PI Bruce JE, Tang X, Garsky V, Brady SF, Li Y, Chen-Dodson E;
PI Sardana M, Shafer JA;

XX DR WPI; 2003-148462/14.

XX PT New beta-secretase substrate peptides, useful as substrates in assays for
PT measuring beta-secretase activity, or for screening test compounds for
PT the ability to inhibit beta-secretase activity used for treating
PT Alzheimer's disease.

XX PS Example 2; Fig 1; 103pp; English.

XX CC The invention relates to a novel substantially pure beta-secretase
CC substrate peptide. A peptide of the invention has neurotrophic, and
CC neuroprotective activity. The peptide acts as a Secretase Inhibitor Beta.
CC The beta-secretase substrate peptides are useful as substrates in various
CC assays for measuring beta-secretase activity. The methods are useful for
CC screening test compounds for the ability to inhibit beta-secretase
CC activity, or inhibiting the cleavage of beta-APP (amyloid precursor
CC protein) in mammalian hosts, which can be used for treating conditions
CC related to amyloid beta peptide deposition, e.g. Alzheimer's disease or
CC Down's syndrome. The present sequence represents a beta secretase
CC substrate peptide of the invention

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 2 VNLDAEF 8

RESULT 38

ABR54162
ID ABR54162 standard; peptide; 8 AA.

XX AC ABR54162;

XX DT 19-JUN-2003 (first entry)

XX DE Beta-secretase substrate peptide #260.

XX KW Beta-secretase; neurotrophic; neuroprotective; Secretase Inhibitor Beta;
KW substrate; beta-APP; amyloid precursor protein; Alzheimer's disease;
KW amyloid beta peptide deposition; Down's syndrome.

XX OS Synthetic.

PI Bruce JE, Tang X, Garsky V, Brady SF, Li Y, Chen-Dodson E;
PI Sardana M, Shafer JA;
XX
XX WPI; 2003-148462/14.
XX
XX New beta-secretase substrate peptides, useful as substrates in assays for
PT measuring beta-secretase activity, or for screening test compounds for
PT the ability to inhibit beta-secretase activity used for treating
PT Alzheimer's disease.
XX
XX
XX Claim 1; Fig 6; 103pp; English.
XX
XX The invention relates to a novel substantially pure beta-secretase
CC substrate peptide. A peptide of the invention has neurotropic, and
CC neuroprotective activity. The peptide acts as a Secretase Inhibitor Beta.
CC The beta-secretase substrate peptides are useful as substrates in various
CC assays for measuring beta-secretase activity. The methods are useful for
CC screening test compounds for the ability to inhibit beta-secretase
CC activity, or inhibiting the cleavage of beta-APP (amyloid precursor
CC protein) in mammalian hosts, which can be used for treating conditions
CC related to amyloid beta peptide deposition, e.g. Alzheimer's disease or
CC Down's syndrome. The present sequence represents a beta secretase
CC substrate peptide of the invention
XX
XX Sequence 8 AA;
SQ

Query Match 100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VNXAAEF 8
|:::|||
|:::|||

RESULT 41
ABR61967
ID ABR61967 standard; peptide; 8 AA.
XX
AC ABR61967;
XX
DT 12-SEP-2003 (first entry)
XX
DE Memapsin 2 protein substrate peptide.
XX
XX Memapsin 1; neurotropic; neuroprotective; memapsin 2; beta secretase;
KW beta-amyloid protein; Alzheimer's disease; promemapsin 2.
XX
XX Synthetic.
XX
XX WO2003039454-A2.
XX
XX 15-MAY-2003.
XX
XX 23-OCT-2002; 2002WO-US034324.
XX
XX 23-OCT-2001; 2001US-0335952P.
XX 27-NOV-2001; 2001US-0333545P.
PR 14-JAN-2002; 2002US-0348464P.
PR 14-JAN-2002; 2002US-0348615P.
PR 20-JUN-2002; 2002US-0390804P.
PR 19-JUL-2002; 2002US-0397557P.
PR 19-JUL-2002; 2002US-0397619P.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
XX Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
PI Turner RT;
XX
XX WPI; 2003-541410/51.
XX
XX New peptide compounds are memapsin beta secretase inhibitors used for

PT treating Alzheimer's disease.
XX
XX Example 5; Page 199; 407pp; English.
XX
XX The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a peptide substrate for memapsin 2
XX
XX Sequence 8 AA;
SQ

Query Match 100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VNLAAEF 8
|:::|||
|:::|||

RESULT 42
ABR61941
ID ABR61941 standard; peptide; 8 AA.
XX
AC ABR61941;
XX
XX 12-SEP-2003 (first entry)
DT
XX
XX Memapsin 2 protein substrate peptide OM99-2.
DE
XX
XX Memapsin 1; neurotropic; neuroprotective; memapsin 2; beta secretase;
KW beta-amyloid protein; Alzheimer's disease; promemapsin 2.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 4..5 /note= "hydroxyethylene linkage"
FT
XX
XX WO2003039454-A2.
XX
XX 15-MAY-2003.
XX
XX 23-OCT-2002; 2002WO-US034324.
XX
XX 23-OCT-2001; 2001US-0335952P.
XX 27-NOV-2001; 2001US-0333545P.
PR 14-JAN-2002; 2002US-0348464P.
PR 14-JAN-2002; 2002US-0348615P.
PR 20-JUN-2002; 2002US-0390804P.
PR 19-JUL-2002; 2002US-0397557P.
PR 19-JUL-2002; 2002US-0397619P.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
XX Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
PI Turner RT;
XX
XX WPI; 2003-541410/51.
XX
XX New peptide compounds are memapsin beta secretase inhibitors used for
PT treating Alzheimer's disease.
XX
XX Example 1; Page 84; 407pp; English.
XX
XX The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a peptide substrate for memapsin 2
XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 6; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 2 VNLAEEF 8

RESULT 43

ABR61936
 ID ABR61936 standard; peptide; 8 AA.

XX AC ABR61936;
 XX DT 12-SEP-2003 (first entry)

XX DE Memapsin 2 protein substrate peptide.
 XX KW Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;

XX KW beta-amyloid protein; Alzheimer's disease; promemapsin 2.
 XX OS Synthetic.

XX PN WO2003039454-A2.
 XX PD 15-MAY-2003.

XX PF 23-OCT-2002; 2002WO-US034324.
 XX PR 23-OCT-2001; 2001US-0335952P.

XX PR 27-NOV-2001; 2001US-033545P.
 XX PR 14-JAN-2002; 2002US-0348464P.

XX PR 14-JAN-2002; 2002US-0348615P.
 XX PR 20-JUN-2002; 2002US-0390804P.

XX PR 19-JUL-2002; 2002US-0397557P.
 XX PR 19-JUL-2002; 2002US-0397619P.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX PA (UNII) UNIV ILLINOIS FOUND.

XX PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
 XX PI Turner RT;

XX DR WPI; 2003-541410/51.
 XX PT New peptide compounds are memapsin beta secretase inhibitors used for

XX PT treating Alzheimer's disease.
 XX PS Example 1; Page 81; 407pp; English.

XX CC The invention relates to peptide compounds of specified formula. The
 XX CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative

XX CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
 XX CC protein. The compounds can be used for treating Alzheimer's disease. The

XX CC present sequence represents a peptide substrate for memapsin 2
 XX SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 6; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 2 VNLAEEF 8

RESULT 44

ABR61945
 ID ABR61945 standard; peptide; 8 AA.

XX ABR61945;
 XX AC 12-SEP-2003 (first entry)

XX DE Memapsin 2 activity inhibiting peptide OM99-2.
 XX KW Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;

XX KW beta-amyloid protein; Alzheimer's disease; promemapsin 2.
 XX OS Synthetic.

XX PH Key Location/Qualifiers
 XX FT Misc-difference 4.5

XX FT /note= "hydroxyethylene transition-state isostere"
 XX PN WO2003039454-A2.

XX PD 15-MAY-2003.
 XX PF 23-OCT-2002; 2002WO-US034324.

XX PR 23-OCT-2001; 2001US-0335952P.
 XX PR 27-NOV-2001; 2001US-033545P.

XX PR 14-JAN-2002; 2002US-0348464P.
 XX PR 14-JAN-2002; 2002US-0348615P.

XX PR 20-JUN-2002; 2002US-0390804P.
 XX PR 19-JUL-2002; 2002US-0397557P.

XX PR 19-JUL-2002; 2002US-0397619P.
 XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PA (UNII) UNIV ILLINOIS FOUND.
 XX PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;

XX PI Turner RT;
 XX DR WPI; 2003-541410/51.

XX PT New peptide compounds are memapsin beta secretase inhibitors used for
 XX PT treating Alzheimer's disease.

XX PS Example 1; Page 91; 407pp; English.
 XX CC The invention relates to peptide compounds of specified formula. The

XX CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
 XX CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid

XX CC protein. The compounds can be used for treating Alzheimer's disease. The
 XX CC present sequence represents a peptide that can inhibit the beta-secretase

XX CC activity of memapsin 2
 XX SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 6; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 2 VNLAEEF 8

RESULT 45

ADA74843
 ID ADA74843 standard; peptide; 8 AA.

XX AC ADA74843;
 XX DT 20-NOV-2003 (first entry)

XX DE OM99-2 peptide inhibitor of human memapsin 2.
 XX KW memapsin 2; beta-secretase; amyloid precursor protein; APP;

XX KW aspartic proteinase 2; ASP2; nootropic; neuroprotective;

```

KW Alzheimer's disease; OM99-2 inhibitor.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 4..5
FT /label= OTHER
FT /note= "OTHER = Leu4 and Ala5 linked by a transition-
FT state isostere (-CH[OH]-CH2-)"
XX
XX
XX US6545127-B1.
XX
XX 08-APR-2003.
XX
XX 27-JUN-2000; 2000US-00604608.
XX
XX 28-JUN-1999; 99US-0141363P.
XX
XX 30-NOV-1999; 99US-0168060P.
XX
XX 25-JAN-2000; 2000US-0177836P.
XX
XX 27-JAN-2000; 2000US-0178368P.
XX
XX 08-JUN-2000; 2000US-0210292P.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JJN, Lin X, Koelsch G, Hong L;
XX WPI; 2003-566587/53.
XX
XX Novel memapsin 2 protein that cleaves a beta-secretase site of an amyloid
XX precursor protein is useful in the design and screening of specific
XX inhibitors for treating and preventing Alzheimer's disease.
XX
XX Example 7; Col 22; 44pp; English.
XX
XX The invention relates to a novel method which comprises the production of
XX purified, catalytically active, recombinant memapsin 2 (beta-secretase)
XX protein where the memapsin protein is expressed in a bacterial cell and
XX cleaves the beta-secretase site of an amyloid precursor protein (APP).
XX Memapsin 2, also known as aspartic proteinase 2 (ASP2), belongs to the
XX aspartic protease family and demonstrates neurotropic and neuroprotective
XX activities. The protein of the invention may be useful in the design and
XX screening of specific inhibitors which are useful in treating and
XX preventing Alzheimer's disease. The current sequence is that of the OM99-
XX 2 peptide inhibitor of human memapsin 2 of the invention.
XX
XX Sequence 8 AA;
XX
Query Match 100.0%; Score 7; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXXAEF 7
Db 2 VNLAAEF 8
|::|||
RESULT 46
ADH34051
ID ADH34051 standard; peptide; 8 AA.
XX
XX ADH34051;
AC
XX 11-MAR-2004 (first entry)
DT
XX
XX Beta-secretase inhibitor 1753.
DE
XX
XX Beta-secretase; BACE; BACE-2; inhibitor; Alzheimer's disease;
KW neuroprotective; neurotropic; amyloid precursor protein;
XX beta-amyloid peptide; cerebrovascular amyloidosis.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH

```

```

FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Leusta (not defined)"
FT Modified-site 8
FT /note= "Amidated and optionally Iodinated"
XX
XX US2003125257-A1.
XX
XX 03-JUL-2003.
XX
XX 18-DEC-2002; 2002US-00322684.
XX
XX 20-DEC-2001; 2001EP-00130282.
XX
XX (BROC/) BROCKHAUS M.
XX (DOEB/) DOEBELI H.
XX (GRUE/) GRUENINGER F.
XX (HUGU/) HUGUENIN P.
XX (KITA/) KITAS E A.
XX (NELB/) NELBOECK-HOCHSTETTER P.
XX
XX Brockhaus M, Doebeli H, Grueninger F, Huguenin P, Kitas EA;
XX Nelboeck-Hochstetter P;
XX WPI; 2004-088811/09.
XX
XX New inhibitors of beta-secretase, useful for treating cerebrovascular
XX amyloidosis, especially Alzheimer's disease, and for drug screening.
XX
XX Disclosure; Fig 5; 23pp; English.
XX
XX The invention relates to peptide beta-secretase (bs) inhibitors of
XX generic formula appearing as ADH34057. Also included are an assay for
XX identifying inhibitors of bs, screening compounds for inhibition of bs
XX activity, a kit for identifying a bs inhibitor and bs inhibitors
XX identified using the kit. The bs used is isolated or recombinant, and
XX purified, especially a full-length bs, specifically BACE or BACE-2. The
XX inhibitors of beta-secretase (which is involved in degradation of amyloid
XX precursor protein to beta-amyloid peptide) are used for treating patients
XX with, or predisposed to, cerebrovascular amyloidosis, specifically
XX Alzheimer's disease. They are also used to prepare tagged derivatives,
XX useful in screening compounds for identifying other bs inhibitors and for
XX radioimaging or positron emission tomographic imaging. The present
XX sequence is a bs inhibitor of the invention.
XX
XX Sequence 8 AA;
XX
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXXAEF 7
Db 2 VNXVAEF 8
|::|||
RESULT 47
ADH34047
ID ADH34047 standard; peptide; 8 AA.
XX
XX ADH34047;
AC
XX 11-MAR-2004 (first entry)
DT
XX
XX Beta-secretase inhibitor 5512.
DE
XX
XX Beta-secretase; BACE; BACE-2; inhibitor; Alzheimer's disease;
KW neuroprotective; neurotropic; amyloid precursor protein;
XX beta-amyloid peptide; cerebrovascular amyloidosis.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH

```

```

FT Misc-difference 4
FT FT /label= OTHER
FT FT /note= "Represented as Alasta or Phesta (not defined) in
FT FT the specification"
FT FT Modified-site 8
FT FT /note= "Amidated"
XX XX US2003125257-A1.
XX XX 03-JUL-2003.
XX PD
XX PD 18-DEC-2002; 2002US-00322684.
XX PF
XX PR 20-DEC-2001; 2001EP-00130282.
XX PA (BROC/) BROCKHAUS M.
XX PA (DOEB/) DOEBELI H.
XX PA (GRUE/) GRUENINGER F.
XX PA (HUGU/) HUGUENIN P.
XX PA (KITA/) KITAS E A.
XX PA (NELB/) NELBOECK-HOCHSTETTER P.
XX XX
XX PI Brockhaus M, Doebeli H, Grueninger F, Huguenin P, Kitas EA;
XX PI Nelboeck-Hochstetter P;
XX XX
XX DR WPI; 2004-088811/09.
XX XX
XX PT New inhibitors of beta-secretase, useful for treating cerebrovascular
XX PT amyloidosis, especially Alzheimer's disease, and for drug screening.
XX XX
XX PS Disclosure; Fig 5; 23pp; English.
XX XX
CC The invention relates to peptide beta-secretase (bs) inhibitors of
CC generic formula appearing as ADH34057. Also included are an assay for
CC identifying inhibitors of bs, screening compounds for inhibition of bs
CC activity, a kit for identifying a bs inhibitor and bs inhibitors
CC identified using the kit. The bs used is isolated or recombinant, and
CC purified, especially a full-length bs, specifically BACE or BACE-2. The
CC inhibitors of beta-secretase (which is involved in degradation of amyloid
CC precursor protein to beta-amyloid peptide) are used for treating patients
CC with, or predisposed to, cerebrovascular amyloidosis, specifically
CC Alzheimer's disease. They are also used to prepare tagged derivatives,
CC useful in screening compounds for identifying other bs inhibitors and for
CC radioimaging or positron emission tomographic imaging. The present
CC sequence is a bs inhibitor of the invention.
XX XX
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 2 VNXVAEEF 8
|:|:|:|:|
|:|:|:|:|

RESULT 48
ADJ71556
ID ADJ71556 standard; peptide; 8 AA.
XX AC ADJ71556;
XX DT 06-MAY-2004 (first entry)
XX DE N-terminal APP peptide C-terminal fragment, SEQ ID 219.
XX XX
XX AC ADJ71556;
XX DT 06-MAY-2004 (first entry)
XX DE N-terminal APP peptide C-terminal fragment, SEQ ID 219.
XX XX
XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
XX KW amyloid precursor protein; APP; Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO2004013172-A2.

Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 1 VKMDAEF 7
|:|:|:|:|
|:|:|:|:|

RESULT 49
ADJ71545
ID ADJ71545 standard; peptide; 8 AA.
XX AC ADJ71545;
XX DT 06-MAY-2004 (first entry)
XX DE N-terminal APP peptide C-terminal fragment, SEQ ID 208.
XX XX
XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
XX KW amyloid precursor protein; APP; Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO2004013172-A2.
XX XX
XX PD 12-FEB-2004.
XX PF
XX PR 18-JUL-2003; 2003WO-EP007833.
XX PR 24-JUL-2002; 2002EP-00447147.
XX PR 06-AUG-2002; 2002US-0401497P.
XX XX
XX PA (INNO-) INNOGENETICS NV.
XX PI Delacourte A, Sergeant N;
XX XX
XX DR WPI; 2004-180423/17.
XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a
XX PT prophylactic vaccine or a therapeutic for preventing or treating a
XX PT disease associated with beta-amyloid formation and/or aggregation, e.g.
XX PT Alzheimer's disease.
XX PS Claim 7; Page 67; 104pp; English.
XX XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX XX
XX SQ Sequence 8 AA;

```

PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

PS Claim 7; Page 67; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

XX Sequence 8 AA;

SQ Query Match 100.0%; Score 7; DB 8; Length 8;

Best Local Similarity 57.1%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 3;

QY 1 VXXXAEEF 7
 |::|||
 Db 2 VKMDAEF 8

RESULT 50

ADJ94379
 ID ADJ94379 standard; peptide; 8 AA.

AC ADJ94379;

XX 03-JUN-2004 (first entry)

XX Human amyloid protein precursor, APP-Sw, beta-secretase cleavage site #4.

XX Human; aspartyl protease; Asp-1; Asp-2(a); Asp-2(b); beta secretase;

KW amyloid protein precursor; APP; Alzheimer's disease; neurotropic;

KW neuroprotective; amyloid beta.

XX Homo sapiens.

XX US6706485-B1.

XX 16-MAR-2004.

XX 12-APR-2000; 2000US-00548376.

XX 24-SEP-1998; 98US-0101594P.

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

XX (PHAA) PHARMACIA & UPJOHN CO.

PA Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

PI WPI; 2004-236722/22.

XX Identifying agents that modulate activity of Asp2 aspartyl protease
 PT useful for treating or preventing Alzheimer's disease involves comparing
 PT APP processing activity of protease in presence and absence of test
 PT agent.

PS Claim 23; SEQ ID NO 67; 109pp; English.

XX The invention relates to identifying agents that modulate activity of
 CC Asp2 (e.g. a beta-secretase, e.g. human Asp-2(b) appearing as ID 6,
 CC encoded by ID 5) aspartyl protease, involves contacting Asp2 with amyloid
 CC precursor protein (APP) in the presence and absence of a test agent,
 CC where Asp2 is a recombinant polypeptide and processes APP into amyloid
 CC beta, determining APP processing activity of Asp2 in presence and absence
 CC of the test agent, and comparing the activities to identify agents that

CC modulate the activity of Asp2. Also disclosed are the cDNA and proteins
 CC for human Asp-1 and Asp-2(a), mouse Asp-2(b), a vector comprising the
 CC nucleic acid encoding Hu-Asp2 protease sequence, a host cell comprising
 CC the vector and the method of producing Hu-Asp polypeptide, an isolated
 CC antibody that specifically binds to Hu-Asp polypeptides, identifying a
 CC cell that can be used to screen for inhibitors of beta secretase
 CC activity, novel isoforms of amyloid protein precursor (APP), where the
 CC last 2 carboxy terminus amino acids of that isoform are both lysine
 CC residues (e.g. those designated APP695-KK or carrying the Swedish
 CC mutation where KM at 595-596 is mutated to NL, designated e.g. APP695-Sw
 CC or APP695-Sw-KK, or a V to F mutation at 642, e.g. APP695-VF, all useful
 CC for assaying for beta secretase activity and screening for inhibitors of
 CC beta-secretase), and polynucleotides that encode the APP proteins. The
 CC method is useful for identifying agents that modulate the activity
 CC (amyloid precursor protein processing activity) of Asp2 aspartyl
 CC protease. Preferably, the method is useful for identifying agents that
 CC inhibit Asp2 aspartyl protease activity. The inhibitors of amyloid
 CC precursor protein processing, are useful for treating or preventing
 CC Alzheimer's disease. The present sequence represents a beta secretase
 CC cleavage site from a human APP protein (as described above) useful for
 CC assaying for beta secretase activity and screening for inhibitors of beta
 CC -secretase.

XX Sequence 8 AA;

SQ Query Match 100.0%; Score 7; DB 8; Length 8;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 |::|||
 Db 2 VKMDAEF 8

RESULT 51

ADOS0475
 ID ADOS0475 standard; peptide; 8 AA.

AC ADOS0475;

XX 29-JUL-2004 (first entry)

XX Substrate peptide #4, to assay beta-secretase activity modulators.

DE Aspartyl protease; Asp; beta secretase; amyloid precursor protein; APP;

KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX US6737510-B1.

XX 18-MAY-2004.

XX 12-APR-2000; 2000US-00548373.

XX 24-SEP-1998; 98US-0101594P.

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

XX (PHAA) PHARMACIA & UPJOHN CO.

PA Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

PI WPI; 2004-387112/36.

XX New Asp2 aspartyl protease protein comprising tripeptides DTG and DSG
 PT involved in processing amyloid precursor protein into amyloid beta,
 PT useful in preparing a composition for treating or preventing Alzheimer's
 PT disease.

PS Disclosure; SEQ ID NO 67; 108pp; English.

XX The invention relates to a method for identifying an agent that decreases
 CC the protease activity of the aspartyl protease (Asp) polypeptide. It also
 CC provides enzyme and enzymatic procedures for cleaving the beta secretase
 CC cleavage site of the amyloid precursor protein (APP). The invention is
 CC useful in preparing a composition for treating or preventing Alzheimer's
 CC disease. It is also useful in gene therapy. The present sequence is a
 CC substrate peptide used to assay beta-secretase activity modulators. This
 CC sequence is used to illustrate the method of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEF 7
 Db 2 VKMDAEF 8
 RESULT 52
 ADR48547
 ID ADR48547 standard; peptide; 8 AA.
 XX
 AC ADR48547;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Peptidomimetic beta secretase inhibitor #1.
 XX
 KW tumour; proliferative disorders; angiogenesis; Cytostatic; Antidiabetic;
 KW Antiangiogenic; Antiinflammatory; Antiarthritic; Antirheumatic;
 KW Antisthmatic; amyloid precursor protein secretases; cancer;
 KW chemotherapy; radiation.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /label= Xaa
 FT /note= "statine"
 XX
 PN WO2004073630-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 18-FEB-2004; 2004WO-US004494.
 XX
 PR 18-FEB-2003; 2003US-0319954P.
 XX
 PA (ROSK-) ROSKAMP RES LLC.
 XX
 XX Paris D, Mullan MJ;
 XX
 DR WPI; 2004-642390/62.
 XX
 XX Use of composition comprising secretase inhibitor in the inhibition of
 PT angiogenesis associated with tumors, proliferative or inflammatory
 PT disorders e.g. leukemia, diabetic retinopathy or osteoarthritis.
 XX
 PS Disclosure; Page 13; 44pp; English.
 XX
 CC The present invention relates to the treatment of tumors or
 CC proliferative disorders; or inhibition of angiogenesis associated with
 CC tumors, proliferative or inflammatory disorders involves administration
 CC of a composition comprising a carrier and at least one secretase
 CC inhibitor. For treatment of tumors (preferably glioblastomas, lung
 CC adenocarcinomas and malignant tumors of the breast, colon, kidney,
 CC bladder, head or neck) or proliferative disorders (preferably
 CC hematopoietic disorders (e.g. leukemias, lymphomas or polycythemia) or
 CC ocular disorders (e.g. diabetic retinopathy, macular degeneration,
 CC glaucoma or retinitis pigmentosa)); or inhibition of angiogenesis

CC associated with tumors, proliferative or inflammatory disorders
 CC (claimed); also in the treatment of rheumatoid arthritis, osteoarthritis,
 CC pulmonary fibrosis, sarcoid granulomas, psoriasis or asthma. The
 CC secretase inhibitor specifically inhibits amyloid precursor protein
 CC secretases. The Abgr1-secretase inhibitor is a peptidomimetic tight
 CC binding transition-state analogue Abgr1-secretase inhibitor. The
 CC composition inhibits the pathological angiogenesis observed in cancer and
 CC other angiogenic-related diseases with minimal side effects; does not
 CC require an extended treatment period and/or combination therapy with
 CC other treatment modalities, such as chemotherapy or radiation. The
 CC present sequence represents a peptidomimetic beta secretase inhibitor, as
 CC a substrate analogue BACE inhibitor.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEF 7
 Db 2 VXXVAEF 8
 RESULT 53
 ADR75388
 ID ADR75388 standard; peptide; 8 AA.
 XX
 AC ADR75388;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Substrate peptide #3, to assay beta-secretase activity.
 XX
 KW Aspartyl protease; Asp; amyloid precursor protein; APP; amyloid beta;
 KW chromosome identification; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN US2004166507-A1.
 XX
 PD 26-AUG-2004.
 XX
 PF 29-AUG-2003; 2003US-00652045.
 XX
 PR 24-SEP-1998; 98US-0101594P.
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 13-OCT-1999; 99US-00416901.
 XX
 PA (GURN/) GURNEY M E.
 PA (BIEN/) BIENKOWAKI M J.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Gurney ME, Bienkowiak MJ, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2004-624916/60.
 XX
 XX Novel purified/isolated polynucleotide encoding polypeptide having
 PT aspartyl protease activity involved in processing amyloid precursor
 PT protein into amyloid beta, useful in identifying agent decreasing
 PT activity of aspartyl protease.
 XX
 XX Disclosure; SEQ ID NO 67; 107pp; English.
 XX
 CC The invention relates to nucleic acid sequences encoding aspartyl
 CC protease (Asp) polypeptides having aspartyl protease activity involved in
 CC processing amyloid precursor protein (APP) into amyloid beta. The
 CC invention also relates to a method for identifying an agent that
 CC decreases the protease activity of the Asp. Asp DNA is useful in
 CC chromosome identification as they can hybridise with a specific location.

CC on a human chromosome and in identifying the relationship between genes
 CC and diseases (particular gene responsible for causing diseases). It is
 CC also useful for identifying candidates to modulate the progression of
 CC Alzheimer's disease. Asp is useful in raising antibodies that are useful
 CC in diagnostic assay for detecting Hu-Asp polypeptide expression. The
 CC present sequence is a substrate peptide used to assay beta-secretase
 CC activity. This sequence is used to illustrate the method of the
 CC invention.

XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 Db 2 VKMDAEF 8
 |.:|:|

RESULT 54
 ADS09430
 ID ADS09430 standard; peptide; 8 AA.
 XX
 AC ADS09430;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 1.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; sAPPa secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-5-methylhexanoic acid"
 XX
 PN WO2004076478-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002438.
 XX
 PR 28-FEB-2003; 2003JP-00052926.
 XX
 PA (KISO/) KISO Y.
 XX
 PI Kiso Y;
 XX
 DR WPI; 2004-661989/64.
 XX
 PT Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Example 1; SEQ ID NO 1; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an sAPPa secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 Db 2 VKMDAEF 8
 |.:|:|

RESULT 56
 ADS09521
 ID ADS09521 standard; peptide; 8 AA.
 XX

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 Db 2 VXXDAEF 8
 |.:|:|

RESULT 55
 ADS09433
 ID ADS09433 standard; peptide; 8 AA.
 XX
 AC ADS09433;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 4.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; sAPPa secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 XX
 PN WO2004076478-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002438.
 XX
 PR 28-FEB-2003; 2003JP-00052926.
 XX
 PA (KISO/) KISO Y.
 XX
 PI Kiso Y;
 XX
 DR WPI; 2004-661989/64.
 XX
 PT Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Example 4; SEQ ID NO 4; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an sAPPa secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 Db 2 VOXDAEF 8
 |.:|:|

RESULT 56
 ADS09521
 ID ADS09521 standard; peptide; 8 AA.
 XX

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AC ADS09521;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Beta-secretase inhibitory peptide - SEQ ID 92.
XX
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX KW cerebral palsy; memory loss; SAPPA secretion promoter;
XX KW neurotropic factor-like agent.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX FT Modified-site 5
XX FT /note= "(R)-1,3-thiazolidine-4-carboxylic acid"
XX
XX PN WO2004076478-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX
XX PS (KISO/) KISO Y.
XX
XX PA Kiso Y;
XX
XX PI WPI; 2004-661989/64.
XX
XX DR Novel compound such as beta-secretase inhibitor, useful as preventive or
XX PT therapeutic agent for treating neurodegenerative disease such as
XX PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX PS Disclosure; SEQ ID NO 92; 143pp; Japanese.
XX
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the
XX prevention or treatment of neurodegenerative diseases, such as:
XX CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX of the invention are also useful in the manufacture of an SAPPA secretion
XX CC promoter or neurotropic factor-like agent. The present amino acid
XX CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX SQ Sequence 8 AA;
XX
XX PS Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 1.8e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXXAEF 7
XX |:|:|:|
XX Db 2 VLXXXXEF 8
XX
XX RESULT 57
XX ADS09436
XX ID ADS09436 standard; peptide; 8 AA.
XX
XX AC ADS09436;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Beta-secretase inhibitory peptide - SEQ ID 7.
XX
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX KW cerebral palsy; memory loss; SAPPA secretion promoter;
XX KW neurotropic factor-like agent.

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XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX
XX PN WO2004076478-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX
XX PA (KISO/) KISO Y.
XX
XX PI Kiso Y;
XX
XX DR WPI; 2004-661989/64.
XX
XX DR Novel compound such as beta-secretase inhibitor, useful as preventive or
XX PT therapeutic agent for treating neurodegenerative disease such as
XX PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX PS Example 7; SEQ ID NO 7; 143pp; Japanese.
XX
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the
XX prevention or treatment of neurodegenerative diseases, such as:
XX CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX of the invention are also useful in the manufacture of an SAPPA secretion
XX CC promoter or neurotropic factor-like agent. The present amino acid
XX CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX SQ Sequence 8 AA;
XX
XX PS Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXXAEF 7
XX |:|:|:|
XX Db 2 VLXXXXEF 8
XX
XX RESULT 58
XX ADS09437
XX ID ADS09437 standard; peptide; 8 AA.
XX
XX AC ADS09437;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Beta-secretase inhibitory peptide - SEQ ID 8.
XX
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX KW cerebral palsy; memory loss; SAPPA secretion promoter;
XX KW neurotropic factor-like agent.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX
XX PN WO2004076478-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-JP002438.

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XX PR 28-FEB-2003; 2003JP-00052926.
XX PA (KISO/) KISO Y.
XX PI Kiso Y;
XX DR WPI; 2004-661989/64.
XX XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX XX
PS Example 8; SEQ ID NO 8; 143pp; Japanese.
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX SQ Sequence 8 AA;
XX Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXNAEF 7
DB 2 VXXNAEF 8
|:|:|
|:|:|
RESULT 59
ADS09449
ID ADS09449 standard; peptide; 8 AA.
XX AC ADS09449;
XX XX
XX DT 02-DEC-2004 (first entry)
XX DE Beta-secretase inhibitory peptide - SEQ ID 20.
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX OS Unidentified.
XX FH Key
XX FT Modified-site 4 Location/Qualifiers
XX FT Modified-site 4 /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX FT Modified-site 5 /note= "(R)-5,5-dimethyl-1,3-thiazolidine-4-carboxylic
XX FT acid"
XX PN WO2004076478-A1.
XX PD 10-SEP-2004.
XX XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX XX
XX PA (KISO/) KISO Y.
XX XX
XX PI Kiso Y;
XX DR WPI; 2004-661989/64.
XX XX
XX PT Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX XX
```

```
XX PS Example 20; SEQ ID NO 20; 143pp; Japanese.
XX XX
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX SQ Sequence 8 AA;
XX Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXNAEF 7
DB 2 VXXNAEF 8
|:|:|
|:|:|
RESULT 60
ADS09452
ID ADS09452 standard; peptide; 8 AA.
XX AC ADS09452;
XX XX
XX DT 02-DEC-2004 (first entry)
XX DE Beta-secretase inhibitory peptide - SEQ ID 23.
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX OS Unidentified.
XX FH Key
XX FT Modified-site 4 Location/Qualifiers
XX FT Modified-site 5 /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX FT Modified-site 5 /note= "(R)-5,5-dimethyl-1,3-thiazolidine-4-carboxylic
XX FT acid"
XX PN WO2004076478-A1.
XX PD 10-SEP-2004.
XX XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX XX
XX PA (KISO/) KISO Y.
XX XX
XX PI Kiso Y;
XX DR WPI; 2004-661989/64.
XX XX
XX PT Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX XX
PS Example 23; SEQ ID NO 23; 143pp; Japanese.
XX XX
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
```

CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred.No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:|||||
 Db 2 VLXAAEF 8

RESULT 61

ADS09444

ID ADS09444 standard; peptide; 8 AA.

XX AC ADS09444;

XX 02-DEC-2004 (first entry)

DE Beta-secretase inhibitory peptide - SEQ ID 15.

XX beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 4

FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"

XX WO2004076478-A1.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-JP002438.

XX 28-FEB-2003; 2003JP-00052926.

XX (KISO/) KISO Y.

XX Kiso Y;

XX WPI; 2004-661989/64.

XX The invention comprises beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 FT Alzheimer's disease, Parkinson's disease and neuropathy.

XX Example 15; SEQ ID NO 15; 143pp; Japanese.

XX The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred.No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:|||||
 Db 2 VLXAAEF 8

RESULT 62

ADS09442

ID ADS09442 standard; peptide; 8 AA.

XX AC ADS09442;

XX 02-DEC-2004 (first entry)

XX Beta-secretase inhibitory peptide - SEQ ID 13.

XX beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 4

FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"

XX WO2004076478-A1.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-JP002438.

XX 28-FEB-2003; 2003JP-00052926.

XX (KISO/) KISO Y.

XX Kiso Y;

XX WPI; 2004-661989/64.

XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 FT Alzheimer's disease, Parkinson's disease and neuropathy.

XX Example 13; SEQ ID NO 13; 143pp; Japanese.

XX The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.

XX Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred.No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:|||||
 Db 2 VLXAAEF 8

RESULT 63

ADS09450

ID ADS09450 standard; peptide; 8 AA.

XX AC ADS09450;

XX 02-DEC-2004 (first entry)

XX Beta-secretase inhibitory peptide - SEQ ID 21.


```

PI Kiso Y;
XX WPI; 2004-661989/64.
XX
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
XX therapeutic agent for treating neurodegenerative disease such as
XX Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 14; SEQ ID NO 14; 143pp; Japanese.
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the
XX prevention or treatment of neurodegenerative diseases, such as:
XX Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX of the invention are also useful in the manufacture of an SAPPA secretion
XX promoter or neurotropic factor-like agent. The present amino acid
XX sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VXXAAEF 7
XX |.:|||
XX 2 VLXNAEF 8
XX
XX Db
XX
XX RESULT 66
XX ADS09448
XX ID ADS09448 standard; peptide; 8 AA.
XX AC ADS09448;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Beta-secretase inhibitory peptide - SEQ ID 19.
XX
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX cerebral palsy; memory loss; SAPPA secretion promoter;
XX neurotropic factor-like agent.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX
XX PN W02004076478-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX
XX PA (KISO/) KISO Y.
XX
XX PI Kiso Y;
XX
XX DR WPI; 2004-661989/64.
XX
XX DR WPI; 2004-661989/64.
XX
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
XX therapeutic agent for treating neurodegenerative disease such as
XX Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 19; SEQ ID NO 19; 143pp; Japanese.
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the

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CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VXXAAEF 7
XX |.:|||
XX 2 VLXNAEF 8
XX
XX Db
XX
XX RESULT 67
XX ADS09499
XX ID ADS09499 standard; peptide; 8 AA.
XX AC ADS09499;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Beta-secretase inhibitory peptide - SEQ ID 70.
XX
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX cerebral palsy; memory loss; SAPPA secretion promoter;
XX neurotropic factor-like agent.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX
XX PN W02004076478-A1.
XX
XX PD 10-SEP-2004.
XX
XX PF 27-FEB-2004; 2004WO-JP002438.
XX
XX PR 28-FEB-2003; 2003JP-00052926.
XX
XX PA (KISO/) KISO Y.
XX
XX PI Kiso Y;
XX
XX DR WPI; 2004-661989/64.
XX
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
XX therapeutic agent for treating neurodegenerative disease such as
XX Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Disclosure; SEQ ID NO 70; 143pp; Japanese.
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the
XX prevention or treatment of neurodegenerative diseases, such as:
XX Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX of the invention are also useful in the manufacture of an SAPPA secretion
XX promoter or neurotropic factor-like agent. The present amino acid
XX sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 7; DB 8; Length 8;
XX Best Local Similarity 71.4%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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XX
XX Example 19; SEQ ID NO 19; 143pp; Japanese.
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
XX secretase inhibitory peptides of the invention are useful for the

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FT Modified-site 4
XX /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
PN WO2004076478-A1.
XX
PD 10-SEP-2004.
XX
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
PA
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
PA
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Disclosure; SEQ ID NO 94; 143pp; Japanese.
PS
XX The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. NO. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 2 VLXDAEF 8
|:|:|
|:|:|
RESULT 71
ADS09467
ID ADS09467 standard; peptide; 8 AA.
AC
XX ADS09467;
XX
XX 02-DEC-2004 (first entry)
DT
XX Beta-secretase inhibitory peptide - SEQ ID 38.
DE
XX beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
FT
XX WO2004076478-A1.
PN
XX 10-SEP-2004.
PD
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
PA
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 41; SEQ ID NO 40; 143pp; Japanese.
PS
XX The invention comprises beta-secretase inhibitory peptides. The beta-

XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 39; SEQ ID NO 38; 143pp; Japanese.
PS
XX The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. NO. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 2 VLXDAEF 8
|:|:|
|:|:|
RESULT 72
ADS09469
ID ADS09469 standard; peptide; 8 AA.
AC
XX ADS09469;
XX
XX 02-DEC-2004 (first entry)
DT
XX Beta-secretase inhibitory peptide - SEQ ID 40.
DE
XX beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
FT
XX WO2004076478-A1.
PN
XX 10-SEP-2004.
PD
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
PA
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 41; SEQ ID NO 40; 143pp; Japanese.
PS
XX The invention comprises beta-secretase inhibitory peptides. The beta-

CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 Db 2 VGXDAAF 8

RESULT 73
 ADS09500
 ID ADS09500 standard; peptide; 8 AA.
 XX
 AC ADS09500;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 71.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.

Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-5-methylhexanoic acid"
 FT
 XX WO2004076478-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002438.
 XX
 PR 28-FEB-2003; 2003JP-00052926.
 XX
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX
 XX WPI; 2004-661989/64.

Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Disclosure; SEQ ID NO 71; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 2 VLXDAAF 8

RESULT 74
 ADS09432
 ID ADS09432 standard; peptide; 8 AA.
 XX
 AC ADS09432;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 3.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.

Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 XX WO2004076478-A1.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-JP002438.
 XX
 PR 28-FEB-2003; 2003JP-00052926.
 XX
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX
 XX WPI; 2004-661989/64.

Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Example 3; SEQ ID NO 3; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 Db 2 VXDAAF 8

RESULT 75
 ADS09451
 ID ADS09451 standard; peptide; 8 AA.
 XX
 AC ADS09451;

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XX 02-DEC-2004 (first entry)
DT Beta-secretase inhibitory peptide - SEQ ID 22.
XX
DE beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
FT
XX WO2004076478-A1.
PN
XX 10-SEP-2004.
PD
XX
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
XX
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Example 22; SEQ ID NO 22; 143pp; Japanese.
PS
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db |::|||
2 VLXQAEF 8

RESULT 76
ADS09502
ID ADS09502 standard; peptide; 8 AA.
AC
XX ADS09502;
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Beta-secretase inhibitory peptide - SEQ ID 73.
DE
XX beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX
XX Unidentified.
OS
XX

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FH Key Location/Qualifiers
FT Modified-site 3
FT /note= "(S)-2-amino-3-(4-thiazole)-propanoic acid"
FT Modified-site 4
FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX
XX WO2004076478-A1.
PN
XX 10-SEP-2004.
PD
XX
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX
XX 28-FEB-2003; 2003JP-00052926.
PR
XX (KISO/) KISO Y.
XX
XX Kiso Y;
PI
XX WPI; 2004-661989/64.
DR
XX
XX Novel compound such as beta-secretase inhibitor, useful as preventive or
PT therapeutic agent for treating neurodegenerative disease such as
PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX
XX Disclosure; SEQ ID NO 73; 143pp; Japanese.
PS
XX
XX The invention comprises beta-secretase inhibitory peptides. The beta-
CC secretase inhibitory peptides of the invention are useful for the
CC prevention or treatment of neurodegenerative diseases, such as:
CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
CC of the invention are also useful in the manufacture of an SAPPA secretion
CC promoter or neurotropic factor-like agent. The present amino acid
CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db |::|||
2 VXXDAEF 8

RESULT 77
ADS09470
ID ADS09470 standard; peptide; 8 AA.
XX
XX ADS09470;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Beta-secretase inhibitory peptide - SEQ ID 41.
DE
XX beta-secretase inhibitory peptide; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
KW cerebral palsy; memory loss; SAPPA secretion promoter;
KW neurotropic factor-like agent.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
FT
XX WO2004076478-A1.
PN
XX 10-SEP-2004.
PD
XX
XX 27-FEB-2004; 2004WO-JP002438.
PF
XX

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PR 28-FEB-2003; 2003JP-00052926.
 XX (KISO/) KISO Y.
 XX Kiso Y;
 PI Kiso Y;
 XX WPI; 2004-661989/64.
 DR
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 XX Example 42; SEQ ID NO 41; 143pp; Japanese.
 PS
 XX The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEP 7
 Db |.:|:|
 2 VLXGAEP 8
 RESULT 78
 ADS09508
 ID ADS09508 standard; peptide; 8 AA.
 XX
 AC ADS09508;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 79.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 FT
 FT WO2004076478-A1.
 PN
 XX
 XX 10-SEP-2004.
 PD
 XX
 XX 27-FEB-2004; 2004WO-JP002438.
 PF
 XX
 XX 28-FEB-2003; 2003JP-00052926.
 PR
 XX (KISO/) KISO Y.
 PA
 PI Kiso Y;
 XX
 XX WPI; 2004-661989/64.
 DR
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX

PS Disclosure; SEQ ID NO 79; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEP 7
 Db |.:|:|
 2 VLXLAEP 8
 RESULT 79
 ADS09518
 ID ADS09518 standard; peptide; 8 AA.
 XX
 AC ADS09518;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Beta-secretase inhibitory peptide - SEQ ID 89.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 3
 FT /note= "(2S)-2-amino-2-(3-tetrahydrofuran-1-yl)-acetic acid"
 FT
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 FT WO2004076478-A1.
 PN
 XX
 XX 10-SEP-2004.
 PD
 XX
 XX 27-FEB-2004; 2004WO-JP002438.
 PF
 XX
 XX 28-FEB-2003; 2003JP-00052926.
 PR
 XX (KISO/) KISO Y.
 PA
 PI Kiso Y;
 XX
 XX WPI; 2004-661989/64.
 DR
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 XX Disclosure; SEQ ID NO 89; 143pp; Japanese.
 PS
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX

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XX SQ Sequence 8 AA;
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VXXDAEF 8

RESULT 80
ADS09434
ID ADS09434 standard; peptide; 8 AA.
XX AC ADS09434;
XX DT 02-DEC-2004 (first entry)
XX DE Beta-secretase inhibitory peptide - SEQ ID 5.
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX KW cerebral palsy; memory loss; SAPPA secretion promoter;
XX KW neurotropic factor-like agent.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
XX PN WO2004076478-A1.
XX PD 10-SEP-2004.
XX PF 27-FEB-2004; 2004WO-JP002438.
XX PR 28-FEB-2003; 2003JP-00052926.
XX XX (KISO/) KISO Y.
XX PI Kiso Y;
XX DR WPI; 2004-661989/64.
XX PT Novel compound such as beta-secretase inhibitor, useful as preventive or
XX PT therapeutic agent for treating neurodegenerative disease such as
XX PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX PS Disclosure; SEQ ID NO 5; 143pp; Japanese.
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
XX CC secretase inhibitory peptides of the invention are useful for the
XX CC prevention or treatment of neurodegenerative diseases, such as:
XX CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX CC of the invention are also useful in the manufacture of an SAPPA secretion
XX CC promoter or neurotropic factor-like agent. The present amino acid
XX CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VXXDAEF 8

RESULT 81
ADS09512
ID ADS09512 standard; peptide; 8 AA.
XX AC ADS09512;
XX DT 02-DEC-2004 (first entry)
XX DE Beta-secretase inhibitory peptide - SEQ ID 83.
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
XX KW cerebral palsy; memory loss; SAPPA secretion promoter;
XX KW neurotropic factor-like agent.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT /note= "(2R, 3S)-3-amino-2-hydroxy-5-methylhexanoic acid"
XX PN WO2004076478-A1.
XX PD 10-SEP-2004.
XX PF 27-FEB-2004; 2004WO-JP002438.
XX PR 28-FEB-2003; 2003JP-00052926.
XX XX (KISO/) KISO Y.
XX PI Kiso Y;
XX DR WPI; 2004-661989/64.
XX PT Novel compound such as beta-secretase inhibitor, useful as preventive or
XX PT therapeutic agent for treating neurodegenerative disease such as
XX PT Alzheimer's disease, Parkinson's disease and neuropathy.
XX PS Disclosure; SEQ ID NO 83; 143pp; Japanese.
XX CC The invention comprises beta-secretase inhibitory peptides. The beta-
XX CC secretase inhibitory peptides of the invention are useful for the
XX CC prevention or treatment of neurodegenerative diseases, such as:
XX CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
XX CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
XX CC of the invention are also useful in the manufacture of an SAPPA secretion
XX CC promoter or neurotropic factor-like agent. The present amino acid
XX CC sequence represents a beta-secretase inhibitory peptide of the invention.
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 7; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 2 VXXDAEF 8

RESULT 82
ADS09446
ID ADS09446 standard; peptide; 8 AA.
XX AC ADS09446;
XX DT 02-DEC-2004 (first entry)
XX DE Beta-secretase inhibitory peptide - SEQ ID 17.
XX KW beta-secretase inhibitory peptide; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;

```

KW cerebral palsy; memory loss; sAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX Unidentified.
 XX OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT Modified-site 5
 FT /note= "(R)-5,5-dimethyl-1,1,3-thiazolidine-4-carboxylic
 FT acid"
 FT
 XX
 XX WO2004076478-A1.
 XX
 XX 10-SEP-2004.
 XX
 XX 27-FEB-2004; 2004WO-JP002438.
 XX
 XX 28-FEB-2003; 2003JP-00052926.
 XX
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX WPI; 2004-661989/64.
 XX
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 XX Example 17; SEQ ID NO 17; 143pp; Japanese.
 XX
 XX The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an sAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 2 VLXXAEF 8
 |::|::|::|
 |::|::|::|
 RESULT 83
 ADS09447
 ID ADS09447 standard; peptide; 8 AA.
 XX AC
 XX ADS09447;
 XX
 XX 02-DEC-2004 (first entry)
 XX
 XX Beta-secretase inhibitory peptide - SEQ ID 18.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; sAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX Unidentified.
 XX OS
 XX Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 XX

PN WO2004076478-A1.
 XX
 XX 10-SEP-2004.
 XX
 XX 27-FEB-2004; 2004WO-JP002438.
 XX
 XX 28-FEB-2003; 2003JP-00052926.
 XX
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX WPI; 2004-661989/64.
 XX
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 XX Example 18; SEQ ID NO 18; 143pp; Japanese.
 XX
 XX The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an sAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 2 VLXDAEF 8
 |::|::|::|
 |::|::|::|
 RESULT 84
 ADS09431
 ID ADS09431 standard; peptide; 8 AA.
 XX AC
 XX ADS09431;
 XX
 XX 02-DEC-2004 (first entry)
 XX
 XX Beta-secretase inhibitory peptide - SEQ ID 2.
 XX
 KW beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; sAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX Unidentified.
 XX OS
 XX Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 XX
 XX WO2004076478-A1.
 XX
 XX 10-SEP-2004.
 XX
 XX 27-FEB-2004; 2004WO-JP002438.
 XX
 XX 28-FEB-2003; 2003JP-00052926.
 XX
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX

DR WPI; 2004-661989/64.
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Example 2; SEQ ID NO 2; 143pp; Japanese.
 XX
 CC The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 PS Sequence 8 AA;
 XX

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 Db 2 VNXDAEF 8
 |.:|:|

RESULT 85
 ADS09435
 ID ADS09435 standard; peptide; 8 AA.
 AC ADS09435;
 XX
 DT 02-DEC-2004 (first entry)
 DE Beta-secretase inhibitory peptide - SEQ ID 6.
 XX beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylbutanoic acid"
 FT
 XX WO2004076478-A1.
 XX 10-SEP-2004.
 XX 27-FEB-2004; 2004WO-JP002438.
 XX 28-FEB-2003; 2003JP-00052926.
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX WPI; 2004-661989/64.
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Example 6; SEQ ID NO 6; 143pp; Japanese.
 XX

The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX

CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 PS Sequence 8 AA;
 XX

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 Db 2 VNXDAEF 8
 |.:|:|

RESULT 86
 ADS09487
 ID ADS09487 standard; peptide; 8 AA.
 AC ADS09487;
 XX
 DT 02-DEC-2004 (first entry)
 DE Beta-secretase inhibitory peptide - SEQ ID 58.
 XX beta-secretase inhibitory peptide; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
 KW cerebral palsy; memory loss; SAPPA secretion promoter;
 KW neurotropic factor-like agent.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "(2R, 3S)-3-amino-2-hydroxy-4-phenylthiobutanoic
 FT acid"
 FT
 XX WO2004076478-A1.
 XX 10-SEP-2004.
 XX 27-FEB-2004; 2004WO-JP002438.
 XX 28-FEB-2003; 2003JP-00052926.
 XX (KISO/) KISO Y.
 XX Kiso Y;
 XX WPI; 2004-661989/64.
 XX Novel compound such as beta-secretase inhibitor, useful as preventive or
 PT therapeutic agent for treating neurodegenerative disease such as
 PT Alzheimer's disease, Parkinson's disease and neuropathy.
 XX
 PS Disclosure; SEQ ID NO 58; 143pp; Japanese.
 XX

The invention comprises beta-secretase inhibitory peptides. The beta-
 CC secretase inhibitory peptides of the invention are useful for the
 CC prevention or treatment of neurodegenerative diseases, such as:
 CC Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis,
 CC cerebral palsy, and memory loss. The beta-secretase inhibitory peptides
 CC of the invention are also useful in the manufacture of an SAPPA secretion
 CC promoter or neurotropic factor-like agent. The present amino acid
 CC sequence represents a beta-secretase inhibitory peptide of the invention.
 XX
 PS Sequence 8 AA;
 XX

Query Match 100.0%; Score 7; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;


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PR 20-FEB-1997; 97US-00802981.
XX (ONCO-) ONCOIMMUNIN INC.
XX Komoriya A, Packard BS;
XX WPI; 1998-467579/40.
XX New fluorogenic compositions - containing 2 fluorophores separated by a
PT peptide comprising a protease binding site, used for detecting protease
PT activity in samples.
XX Claim 4; Page 77; 90pp; English.
XX
XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
CC composition which is used for the detection of protease activity in
CC biological samples. The products can be used for the detection of
CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,
CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
CC steroids or polymers. In addition, attachment of a hydrophobic group to a
CC molecule can be used to enhance uptake by cells. The composition is
CC composed of P = peptide comprising a protease binding site for the
CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
CC amino terminal amino acid and F2 is attached to the carboxyl terminal
CC amino acid and S1, S2 peptides = when present, are peptide spacers where
CC S1, when present, is attached to the amino terminal acid, and S2, when
CC present, is attached to the carboxyl terminal amino acid
XX
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 7; DB 2; Length 9;
XX Best Local Similarity 57.1%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXAAEF 7
XX Db 3 VKLDAEF 9
XX
XX RESULT 90
XX AAY87949
XX ID AAY87949 standard; protein; 9 AA.
XX AC AAY87949;
XX DT 11-SEP-2000 (first entry)
XX DE Mammalian amyloid precursor protein substrate peptide.
XX KW Amyloid precursor protein; APP; secretase; vesicle; Abeta peptide;
XX KW Alzheimer's disease.
XX OS Mammalia.
XX PI XX
XX PN WO200023576-A2.
XX PD 27-APR-2000.
XX PF 15-OCT-1999; 99WO-US024403.
XX PR 16-OCT-1998; 98US-00173887.
XX PR 20-APR-1999; 99US-00294987.
XX
XX (HOOK/) HOOK V Y H.
XX
XX Hook VYH;
XX
XX WPI; 2000-339679/29.
XX
XX Determining the proteolytic activity of secretase for treating
PT Alzheimer's disease comprises permeabilizing vesicles and incubating with
PT amyloid precursor protein (APP) to determine cleavage of APP substrate.
XX

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PS Example XV; Page 97; 97pp; English.
XX
XX This invention describes a novel method for the determination of the
CC proteolytic activity of a secretase comprising obtaining and
CC permeabilizing pure vesicles, incubating the vesicles with an amyloid
CC precursor protein (APP) and determining the cleavage of the APP substrate
CC where the amount of cleavage is proportional to the proteolytic activity
CC of the secretase. The methods are useful for selecting secretases and
CC agents that cleave the amyloid precursor protein substrate, inhibiting
CC production of the Abeta peptide found in Alzheimer's disease and treating
CC Alzheimer's disease in patients. This sequence represents a mammalian
CC amyloid precursor protein, APP substrate which is used in the method of
CC the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 7; DB 3; Length 9;
XX Best Local Similarity 57.1%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXAAEF 7
XX Db 3 VKMDAEF 9
XX
XX RESULT 91
XX AAB07876
XX ID AAB07876 standard; peptide; 9 AA.
XX AC AAB07876;
XX DT 14-NOV-2000 (first entry)
XX DE A peptide fragment derived from beta-amyloid precursor protein.
XX
XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
XX KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
XX KW inhibitor.
XX OS Homo sapiens.
XX PN WO2000047618-A2.
XX PD 17-AUG-2000.
XX PF 10-FEB-2000; 2000WO-US003819.
XX PR 10-FEB-1999; 99US-0119571P.
XX PR 15-JUN-1999; 99US-0139172P.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
XX Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
XX WPI; 2000-533011/48.
XX
XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
XX
XX Disclosure; Page 12; 121pp; English.
XX
XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein
XX

```


CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 3; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 Db 3 VNFLAEF 9
 |:::|

RESULT 97
 AAB07878
 ID AAB07878 standard; peptide; 9 AA.
 AC AAB07878;
 XX
 XX 14-NOV-2000 (first entry)

DE A peptide fragment derived from beta-amyloid precursor protein.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.
 XX Homo sapiens.
 OS
 XX WO200047618-A2.
 PN
 XX 17-AUG-2000.

PF 10-FEB-2000; 2000WO-US003819.
 XX
 XX 10-FEB-1999; 99US-0119571P.
 PR
 PR 15-JUN-1999; 99US-0139172P.
 XX

PA (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 XX WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.

PS Disclosure; Page 12; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 3; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 Db 3 VKVAAEF 9
 |:::|

DT 14-NOV-2000 (first entry)

XX A peptide fragment derived from beta-amyloid precursor protein.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.
 XX Homo sapiens.
 OS
 XX WO200047618-A2.
 PN
 XX 17-AUG-2000.

PF 10-FEB-2000; 2000WO-US003819.

XX 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 XX WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.

PS Disclosure; Page 12; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 3; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 Db 3 VKLDAEF 9
 |:::|

RESULT 99

AAB07877

ID AAB07877 standard; peptide; 9 AA.

XX

AC AAB07877;

XX

DT 14-NOV-2000 (first entry)
 XX A peptide fragment derived from beta-amyloid precursor protein.
 DE
 XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.
 XX Homo sapiens.
 OS
 XX WO200047618-A2.
 PN
 XX
 XX 17-AUG-2000.
 PD
 XX 10-FEB-2000; 2000WO-US003819.
 PF
 XX 10-FEB-1999; 99US-0119571P.
 PR
 XX 15-JUN-1999; 99US-0139172P.
 PR
 XX (ELAN-) ELAN PHARM INC.
 PA
 XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 PI
 XX WPI; 2000-533011/48.
 XX
 XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 PT
 XX Disclosure; Page 12; 121pp; English.
 PS
 XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 7; DB 3; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 DB |::|||
 3 VNFDAEF 9
 RESULT 100
 AAB07880
 ID AAB07880 standard; peptide; 9 AA.
 XX
 AC AAB07880;
 XX
 XX 14-NOV-2000 (first entry)
 DT
 XX A peptide fragment derived from beta-amyloid precursor protein.
 DE
 XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.
 XX Homo sapiens.
 OS
 XX WO200047618-A2.
 PN
 XX
 XX 17-AUG-2000.
 PD

XX 10-FEB-2000; 2000WO-US003819.
 PF
 XX 10-FEB-1999; 99US-0119571P.
 PR
 XX 15-JUN-1999; 99US-0139172P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA
 XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 PI
 XX WPI; 2000-533011/48.
 XX
 XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 PT
 XX Disclosure; Page 12; 121pp; English.
 PS
 XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 7; DB 3; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 DB |::|||
 3 VKLAEEF 9
 RESULT 101
 AAB07879
 ID AAB07879 standard; peptide; 9 AA.
 XX
 AC AAB07879;
 XX
 XX 14-NOV-2000 (first entry)
 DT
 XX A peptide fragment derived from beta-amyloid precursor protein.
 DE
 XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor.
 XX Homo sapiens.
 OS
 XX WO200047618-A2.
 PN
 XX
 XX 17-AUG-2000.
 PD
 XX 10-FEB-2000; 2000WO-US003819.
 PF
 XX 10-FEB-1999; 99US-0119571P.
 PR
 XX 15-JUN-1999; 99US-0139172P.
 PR
 XX (ELAN-) ELAN PHARM INC.
 PA
 XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 PI
 XX WPI; 2000-533011/48.
 XX
 XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 PT
 XX Disclosure; Page 12; 121pp; English.
 PS
 XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX
 XX Sequence 9 AA;
 SQ

PT Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
XX
XX Disclosure; Page 12; 121pp; English.
XX
XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
|::|||
Db 3 VNLAEEF 9
|::|||
RESULT 102
AAB07881
ID AAB07881 standard; peptide; 9 AA.
XX
XX AAB07881;
AC
XX
XX 14-NOV-2000 (first entry)
DT
XX A peptide fragment derived from beta-amyloid precursor protein.
DE
XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
XX amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.
KW
XX Homo sapiens.
OS
XX WO200047618-A2.
PN
XX 17-AUG-2000.
PD
XX 10-FEB-2000; 2000WO-US003819.
PF
XX 10-FEB-1999; 99US-0119571P.
PR
XX 15-JUN-1999; 99US-0139172P.
PR
XX (ELAN-) ELAN PHARM INC.
PA
XX
XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
PI
XX WPI; 2000-533011/48.
DR
XX
XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
PT
XX Disclosure; Page 12; 121pp; English.
XX
XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or

CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
|::|||
Db 3 VKMLAEF 9
|::|||
RESULT 103
AAB07883
ID AAB07883 standard; peptide; 9 AA.
XX
XX AAB07883;
AC
XX
XX 14-NOV-2000 (first entry)
DT
XX A peptide fragment derived from beta-amyloid precursor protein.
DE
XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.
KW
XX Homo sapiens.
OS
XX WO200047618-A2.
PN
XX 17-AUG-2000.
PD
XX 10-FEB-2000; 2000WO-US003819.
PF
XX 10-FEB-1999; 99US-0119571P.
PR
XX 15-JUN-1999; 99US-0139172P.
PR
XX (ELAN-) ELAN PHARM INC.
PA
XX
XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
PI
XX WPI; 2000-533011/48.
DR
XX
XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
PT
XX Disclosure; Page 12; 121pp; English.
XX
XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
|::|||
Db 3 VKMLAEF 9
|::|||

RESULT 104

AAB07885
ID AAB07885 standard; peptide; 9 AA.

AC AAB07885;

DT 14-NOV-2000 (first entry)

DE A peptide fragment derived from beta-amyloid precursor protein.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.

XX Homo sapiens.

PN WO200047618-A2.

PD 17-AUG-2000.

PF 10-FEB-2000; 2000WO-US003819.

PR 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

DR WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.

XX Disclosure; Page 12; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

DB |:::|
3 VNFAAEF 9

RESULT 105

AAB07882

ID AAB07882 standard; peptide; 9 AA.

AC AAB07882;

DT 14-NOV-2000 (first entry)

DE A peptide fragment derived from beta-amyloid precursor protein.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.

OS Homo sapiens.

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US003819.

XX 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.

PS Disclosure; Page 12; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide derived from beta-amyloid precursor protein

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

DB |:::|
3 VNLLAEF 9

RESULT 106

AAB07894

ID AAB07894 standard; peptide; 9 AA.

XX AAB07894;

XX 14-NOV-2000 (first entry)

DE Substrate for beta-secretase enzyme.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.

OS Synthetic.

XX Key Location/Qualifiers

XX Cleavage-site 5..6

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US003819.

```

XX 10-FEB-1999; 99US-0119571P.
PR 15-JUN-1999; 99US-0139172P.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
XX
XX WPI; 2000-533011/48.
XX
XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
XX
XX Example 4; Page 71; 121pp; English.
XX
XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a peptide substrate used to test the activity of beta-
CC secretase enzyme
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
Db |::|||
3 VKLDAEF 9
RESULT 107
AAG73293
ID AAG73293 standard; peptide; 9 AA.
XX
XX AAG73293;
XX
XX 14-AUG-2001 (first entry)
XX
XX Protease indicator compound peptide #22.
XX
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT
FT WO200118238-A1.
XX
XX 15-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-US024882.
XX
XX 10-SEP-1999; 99US-00394019.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Komoriya A, Packard BS;
XX
XX WPI; 2001-389573/41.
XX
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT

```

```

XX Komoriya A, Packard BS;
PI
XX WPI; 2001-389573/41.
XX
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
XX Claim 1; Page 70; 86pp; English.
XX
XX The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
Db |::|||
3 VKLDAEF 9
RESULT 108
AAG73280
ID AAG73280 standard; peptide; 9 AA.
XX
XX AAG73280;
XX
XX 14-AUG-2001 (first entry)
XX
XX Protease indicator compound peptide #9.
XX
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT
FT WO200118238-A1.
XX
XX 15-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-US024882.
XX
XX 10-SEP-1999; 99US-00394019.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Komoriya A, Packard BS;
XX
XX WPI; 2001-389573/41.
XX
XX New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT

```



```
PT samples.
XX
PS Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
|::|||

RESULT 109
AAG73279
ID AAG73279 standard; peptide; 9 AA.
XX
AC AAG73279;
XX
DT 14-AUG-2001 (first entry)
XX
DE Protease indicator compound peptide #8.
XX
KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
PN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-US024882.
XX
PR 10-SEP-1999; 99US-00394019.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 2001-389573/41.
XX
PT New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
PS Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
|::|||

RESULT 110
AAG73297
ID AAG73297 standard; peptide; 9 AA.
XX
AC AAG73297;
XX
DT 14-AUG-2001 (first entry)
XX
DE Protease indicator compound peptide #26.
XX
KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
PN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-US024882.
XX
PR 10-SEP-1999; 99US-00394019.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 2001-389573/41.
XX
PT New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
PS Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
|::|||

RESULT 111
ABB06519
ID ABB06519 standard; peptide; 9 AA.
XX
AC ABB06519;
XX
DT 31-MAY-2002 (first entry)
XX
```

```
PT samples.
XX
PS Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
|::|||

RESULT 110
AAG73297
ID AAG73297 standard; peptide; 9 AA.
XX
AC AAG73297;
XX
DT 14-AUG-2001 (first entry)
XX
DE Protease indicator compound peptide #26.
XX
KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
KW haemophilia.
XX
OS Synthetic.
XX
PN WO200118238-A1.
XX
PD 15-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-US024882.
XX
PR 10-SEP-1999; 99US-00394019.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 2001-389573/41.
XX
PT New fluorogenic compositions whose fluorescence level increases in the
PT presence of active proteases, useful for detecting and localizing
PT protease activity in biological samples, particularly in frozen tissue
PT samples.
XX
PS Claim 1; Page 70; 86pp; English.
XX
CC The present invention describes fluorogenic compositions which can be
CC used for the detection of protease activity. This can be useful as an
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
CC thrombosis and arthritis. The fluorogenic compositions comprise a
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
CC peptide is cleaved by a protease and the fluorophores can then be
CC detected. The present sequence is one of the peptides described in the
CC exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
|::|||

RESULT 111
ABB06519
ID ABB06519 standard; peptide; 9 AA.
XX
AC ABB06519;
XX
DT 31-MAY-2002 (first entry)
XX
```

```

DE  Beta-secretase related peptide SEQ ID NO:113.
XX
KW  Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW  aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
XX  Alzheimer's disease.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200206306-A2.
XX
PD  24-JAN-2002.
XX
XX  19-JUL-2001; 2001WO-US023035.
XX
XX  19-JUL-2000; 2000US-0219795P.
XX  12-MAR-2001; 2001US-0275251P.
XX
XX  (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX  Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI  Heinrichson RL;
XX
XX  WPI; 2002-216995/27.
XX
XX  Novel substrates for human aspartyl protease useful for identifying
PT  modulators of beta secretase activity of aspartyl protease for treating
PT  Alzheimer's disease.
XX
XX  Disclosure; Page 156; 188pp; English.
XX
CC  The present invention describes an isolated peptide (I) comprising a
CC  sequence of at least four amino acids, where the peptide is a substrate
CC  for conducting aspartyl protease assays. (I) has neuroprotective and
CC  nootropic activities, and can be used as an inhibitor of beta-secretase
CC  activity. A beta-secretase modulator from the present invention can be
CC  used for inhibiting beta-secretase activity in vivo, and in the
CC  manufacture of a medicament for the treatment of Alzheimer's disease.
CC  Pharmaceutical compositions from the present invention can be used for
CC  treating a disease or condition characterised by an abnormal beta-
CC  secretase activity. (I) is useful for identifying agents that modulate
CC  the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
CC  a core structure to construct derivatives. ABU49914 to ABU49925 and
CC  ABB06409 to ABB06593 represent sequences used in the exemplification of
CC  the present invention
XX
SQ  Sequence 9 AA;

Query Match      100.0%; Score 7; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY  1 VXXAAEF 7
    |::|||
Db  2 VNLDAEF 8

RESULT 112
ABB09003
ID  ABB09003 standard; peptide; 9 AA.
XX
AC  ABB09003;
XX
XX  19-JUN-2002 (first entry)
XX
XX  Peptide #1 used as a tag to identify cleavage products.
XX
KW  Amyloid precursor protein; APP; Alzheimer's disease; nootropic;
KW  neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
KW  Down's syndrome; cerebral amyloid angiopathy; dementia.
XX
OS  Synthetic.
XX

```

```

FH  Key      Location/Qualifiers
FT  Cleavage-site 5..6
FT  /note= "Beta secretase cleavage site"
XX
PN  WO200202505-A2.
XX
PD  10-JAN-2002.
XX
XX  29-JUN-2001; 2001WO-US020852.
XX
XX  30-JUN-2000; 2000US-0215323P.
XX
XX  (ELAN-) ELAN PHARM INC.
XX
XX  Fang LY, Hom R, John V, Maillaird M;
XX  WPI; 2002-171625/22.
XX
XX  New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
PT  for treating Alzheimer's disease, mild cognitive impairment and Down's
PT  syndrome.
XX
XX  Example D; Page 96; 136pp; English.
XX
XX  This invention relates to substituted amines and their salts, which are
CC  nootropic, neuroprotective, cerebroprotective, haemostatic and
CC  antiparkinsonian in their action. They are used in the preparation of a
CC  composition useful for treating, preventing or delaying the on-set of
CC  Alzheimer's disease, for treating mild cognitive impairment, Down's
CC  syndrome, cerebral amyloid angiopathy, dementia associated with
CC  Parkinson's disease, dementia associated with progressive supranuclear
CC  palsy, and dementia associated with cortical basal degeneration. They are
CC  also useful for treating diseases characterised by beta-amyloid deposits
CC  in brain, and for producing beta-secretase complexes. This sequence
CC  represents a peptide that incorporate the known cleavage site of beta-
CC  secretase. This substrate is used to assay beta-secretase activity
XX
SQ  Sequence 9 AA;

Query Match      100.0%; Score 7; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY  1 VXXAAEF 7
    |::|||
Db  3 VNLDAEF 9

RESULT 113
ABU60428
ID  ABU60428 standard; peptide; 9 AA.
XX
XX  ABU60428;
XX
XX  29-APR-2003 (first entry)
XX
XX  Protease binding peptide motif SEQ ID 137.
XX
XX  Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW  nuclease; screening; fluorophore; substrate cleavage.
XX
XX  Synthetic.
XX
XX  WO200261038-A2.
XX
XX  08-AUG-2002.
XX
XX  21-DEC-2001; 2001WO-US049781.
XX
XX  22-DEC-2000; 2000US-00747287.
XX
XX  (ONCO-) ONCOIMMUNIN INC.
XX

```

PI Packard BS, Komoriya A;
 DR WPI; 2002-698548/75.
 XX
 XX
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 XX
 XX Disclosure; Page 34; 97pp; English.
 PS
 XX
 XX This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorene-carboxylic group, 9-fluorene-carboxylic group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzene-sulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db |:::|
 3 VKLDAEF 9
 RESULT 114
 ID ABU60430 standard; peptide; 9 AA.
 AC ABU60430;
 XX
 XX 29-APR-2003 (first entry)
 DE Protease binding peptide motif SEQ ID 142.
 XX
 XX Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX

OS Synthetic.
 XX WO200261038-A2.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 21-DEC-2001; 2001WO-US049781.
 PF
 XX
 XX 22-DEC-2000; 2000US-00747287.
 PR
 XX
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX
 XX Packard BS, Komoriya A;
 PI
 XX
 XX WPI; 2002-698548/75.
 DR
 XX
 XX Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 XX Disclosure; Page 34; 97pp; English.
 PS
 XX
 XX This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
 CC fluorene-carboxylic group, 9-fluorene-carboxylic group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
 CC benzene-sulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db |:::|
 3 VKMDAEF 9
 RESULT 115

ABU60429
ID ABU60429 standard; peptide; 9 AA.
XX
AC ABU60429;
XX
DT 29-APR-2003 (first entry)
XX
XX
DE Protease binding peptide motif SEQ ID 139.
XX
XX
KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW nuclease; screening; fluorophore; substrate cleavage.
XX
XX
OS Synthetic.
XX
PN WO200261038-A2.
XX
XX 08-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-US049781.
XX
XX 22-DEC-2000; 2000US-00747287.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX
XX WPI; 2002-698548/75.
XX
XX
XX Indicator composition comprising polypeptide or nucleic acid backbone
PT joining two same chromophores resulting in quenching of fluorescence
PT of/change in absorbance of chromophores, useful for detecting protease
PT activity.
XX
XX
PS Disclosure; Page 34; 97pp; English.
XX
XX
CC This invention describes a novel indicator composition (referred as homo-
CC doubly labeled compositions) comprising a polypeptide backbone or a
CC nucleic acid backbone joining two chromophores of the same species
CC whereby the chromophores form an H-dimer resulting in quenching of the
CC fluorescence of or a change in the absorbance of the chromophore, a
CC decrease in fluorescence or a change in absorbance indicates that the
CC first molecule and the second molecule are interacting. The indicator is
CC useful for detecting the activity of a protease, where an increase in
CC fluorescence or a change in absorbance indicates that the protease
CC cleaves the polypeptide backbone. The indicator is attached to a solid
CC support inside a mammalian, yeast or insect cell. The composition bears a
CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-
CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
CC useful for detecting protease or nuclease activity (or the presence of
CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
CC cultured adherent cells), a biological sample such as tissue, biopsy,
CC lymph, embryo, or whole animal, or cell suspension derived from a
CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
CC The indicator composition is also useful for screening a test agent for
CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
CC indicator reagents allow rapid determination of protease activity in a
CC matter of minutes in a single-step procedure. The fluorescent indicators
CC both absorb and emit in the visible range (400-800 nm). These signals are
CC therefore not readily quenched by, nor is activation of the fluorophores,
CC that is, absorption of light, interfered with by background molecules;
CC therefore they are easily detected in biological samples. The fluorogenic
CC protease indicators utilize high efficiency fluorophores and are able to
CC achieve a high degree of quenching while providing a strong signal when
CC the quench is released by cleavage of the peptide substrate. The high
CC signal allows detection of very low levels of protease activity. Thus the
CC fluorogenic protease indicators are particularly well suited for in situ
CC detection of protease activity. ABU60357-ABU60477 represent peptides use
CC to illustrate the method described in the disclosure of the invention

SQ Sequence 9 AA;
Query Match 100.0%; Score 7; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEP 7
DB 3 VNLDAP 9
RESULT 116
ABU60441
ID ABU60441 standard; peptide; 9 AA.
XX
AC ABU60441;
XX
DT 29-APR-2003 (first entry)
XX
DE Protease binding peptide motif SEQ ID 165.
XX
XX
KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
KW nuclease; screening; fluorophore; substrate cleavage.
XX
XX Synthetic.
XX
PN WO200261038-A2.
XX
XX 08-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-US049781.
XX
XX 22-DEC-2000; 2000US-00747287.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX
XX WPI; 2002-698548/75.
XX
XX
XX Indicator composition comprising polypeptide or nucleic acid backbone
PT joining two same chromophores resulting in quenching of fluorescence
PT of/change in absorbance of chromophores, useful for detecting protease
PT activity.
XX
XX
PS Disclosure; Page 35; 97pp; English.
XX
XX
CC This invention describes a novel indicator composition (referred as homo-
CC doubly labeled compositions) comprising a polypeptide backbone or a
CC nucleic acid backbone joining two chromophores of the same species
CC whereby the chromophores form an H-dimer resulting in quenching of the
CC fluorescence of or a change in the absorbance of the chromophore, a
CC decrease in fluorescence or a change in absorbance indicates that the
CC first molecule and the second molecule are interacting. The indicator is
CC useful for detecting the activity of a protease, where an increase in
CC fluorescence or a change in absorbance indicates that the protease
CC cleaves the polypeptide backbone. The indicator is attached to a solid
CC support inside a mammalian, yeast or insect cell. The composition bears a
CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-
CC fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-
CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-
CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
CC useful for detecting protease or nuclease activity (or the presence of
CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
CC cultured adherent cells), a biological sample such as tissue, biopsy,
CC lymph, embryo, or whole animal, or cell suspension derived from a
CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
CC The indicator composition is also useful for screening a test agent for
CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
CC indicator reagents allow rapid determination of protease activity in a
CC matter of minutes in a single-step procedure. The fluorescent indicators

CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilise high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |::|||
 Db 3 VNLDAEF 9

RESULT 117

AAE16663
 ID AAE16663 standard; peptide; 9 AA.

XX AC AAE16663;

XX DT 09-APR-2002 (first entry)

XX DE Oligopeptide substrate #1, used in the assay of the invention.

XX KW Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
 KW degenerative disease; beta-amyloid deposit; mild cognitive impairment;
 KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
 KW cerebral amyloid angiopathy; Parkinson's disease; supranuclear palsy;
 KW cortical basal degeneration; AD; MCI; amyloid precursor protein;
 KW beta-secretase; amyloid beta peptide; A beta peptide.

XX OS Unidentified.

XX FH Key Location/Qualifiers
 FT Cleavage-site 5.6

XX PN WO200202518-A2.

XX PD 10-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US020856.

XX PR 30-JUN-2000; 2000US-0215323P.

XX PA (ELAN-) ELAN PHARM INC.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;

XX DR WPI; 2002-122550/16.

XX FT New substituted amine derivatives, useful for treating Alzheimer's
 PT disease and other degenerative diseases.

XX PS Example D; Page 163; 286pp; English.

XX CC The invention relates to disubstituted amine derivative compounds useful
 CC for treating Alzheimer's disease and other degenerative diseases.
 CC Compounds of the invention possess beta secretase inhibitory activity and
 CC are useful for inhibiting beta-secretase mediated cleavage of amyloid
 CC precursor protein (APP) and particularly, to inhibit the production of
 CC amyloid beta (A beta) peptide. They are useful for treating or preventing
 CC a disease characterised by beta-amyloid deposits in the brain e.g. for
 CC treating or preventing Alzheimer's disease (AD), for helping to prevent

CC or delay the onset of Alzheimer's disease, for treating mild cognitive
 CC impairment (MCI), Down's syndrome, hereditary cerebral haemorrhage with
 CC the amyloidosis of the Dutch type, cerebral amyloid angiopathy and
 CC preventing its potential consequences i.e. single and recurrent lobar
 CC haemorrhages, for treating other degenerative dementias including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration
 CC and diffuse Lewy body type of Alzheimer's disease. The present sequence
 CC is oligopeptide substrate used in assay of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |::|||
 Db 3 VNLDAEF 9

RESULT 118

AAU74837

ID AAU74837 standard; peptide; 9 AA.

XX AC AAU74837;

XX DT 09-SEP-2004 (revised)

XX DT 09-APR-2002 (first entry)

XX DE Synthetic amyloid precursor protein (APP) oligopeptide substrate #1.

XX KW Amyloid precursor protein; APP; Alzheimer's disease; amine XV; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
 KW beta-secretase; amyloid beta peptide; amyloidosis; beta-amyloid plaque;
 KW mild cognitive impairment; MCI; Down's syndrome;
 KW hereditary cerebral haemorrhage; cortical basal degeneration;
 KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;
 KW Parkinson's disease; supranuclear palsy; dementia.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Cleavage-site 5.6
 FT /note= "Beta-secretase cleavage site"

XX PN WO200202506-A2.

XX PD 10-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US020930.

XX PR 30-JUN-2000; 2000US-0215323P.

XX PA (ELAN-) ELAN PHARM INC.

XX PI Fang LY, John V;

XX DR WPI; 2002-147995/19.

XX FT New substituted amines are e.g. amyloid beta peptide production
 PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
 PT mild cognitive impairment and other degenerative diseases.

XX PS Example D; Page 118; 434pp; English.

XX CC This invention relates to a novel substituted amine of formula XV and its
 CC salts which can be used to treat Alzheimer's disease and similar
 CC diseases. The compound of the invention may have nootropic,
 CC neuroprotective, cerebroprotective, haemostatic and antiparkinsonian
 CC activities. The amine acts as a beta-secretase activity inhibitor,
 CC inhibiting cleavage of amyloid precursor protein (APP) and the formation

CC of amyloid beta peptide and beta-amyloid plaque production. The amine of
 CC the invention is useful for treating or preventing a disease
 CC characterised by beta-amyloid deposits in the brain e.g. Alzheimer's
 CC disease (AD), for treating mild cognitive impairment (MCI), preventing or
 CC delaying the onset of Alzheimer's disease in those who would progress
 CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
 CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, dementia associated with cortical basal
 CC degeneration and diffuse Lewy body type of Alzheimer's disease. The
 CC present sequence represents a synthetic APP oligopeptide substrate #1 for
 CC the beta secretase enzyme. This synthetic substrate was used to test the
 CC efficiency of the amine as an inhibitor of beta secretase enzyme activity
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 119
 ABB07598
 ID ABB07598 standard; peptide; 9 AA.
 AC ABB07598;
 XX
 XX 08-MAY-2002 (first entry)
 DT
 XX
 DE Synthetic oligopeptide substrate having beta-secretase cleavage site.
 XX
 KW APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;
 KW amyloid beta peptide; beta-amyloid; nootropic; neuroprotective;
 KW cerebroprotective; haemostatic; antiparkinsonian.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 5..6
 FT /note= "beta-secretase cleavage site"
 XX
 XX WO200202520-A2.
 PN
 XX 10-JAN-2002.
 PD
 XX
 XX 02-JUL-2001; 2001WO-US021000.
 PF
 XX 30-JUN-2000; 2000US-0215323P.
 PR 29-JUN-2001; 2001US-00895843.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;
 PI WPI; 2002-188416/24.
 XX
 DR New disubstituted amine derivatives, useful for treating Alzheimer's
 XX disease and other degenerative diseases.
 PT
 XX Example D; Page 163; 286pp; English.
 PS
 XX The invention relates to disubstituted amine derivatives of specified
 CC formulae or their salts. The amine derivatives can inhibit beta-secretase

CC activity or inhibit the cleavage of amyloid precursor protein (APP) in a
 CC reaction mixture. They can also be used to inhibit production of amyloid
 CC beta peptide (A beta) in a cell or inhibit production of beta-amyloid
 CC plaque in an animal. The amine derivatives are useful for treating or
 CC preventing a disease characterized by beta-amyloid deposits in the brain
 CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
 CC prevent or delay the onset of AD, for treating mild cognitive impairment
 CC (MCI), preventing or delaying the onset of AD in those who would progress
 CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
 CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, dementia associated with cortical basal
 CC degeneration, diffuse Lewy body type of Alzheimer's disease. Sequences
 CC ABB07598-599 are synthetic APP oligopeptide substrates containing the
 CC cleavage site of beta-secretase, used to assay beta-secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 120
 AAM50897
 ID AAM50897 standard; peptide; 9 AA.
 XX
 AC AAM50897;
 XX
 XX 07-MAY-2002 (first entry)
 DT
 XX
 DE Oligopeptide substrate for beta-secretase.
 XX
 KW Beta-secretase; substrate; amyloid precursor protein; APP;
 KW amyloid beta peptide; inhibitor; screening; neurodegenerative disorder;
 KW cognitive impairment; Down's syndrome; Alzheimer's disease;
 KW hereditary cerebral haemorrhage; cerebral amyloid angiopathy; dementia;
 KW therapy.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 5..6
 XX
 XX WO200202512-A2.
 PN
 XX 10-JAN-2002.
 PD
 XX
 XX 29-JUN-2001; 2001WO-US021012.
 PF
 XX 30-JUN-2000; 2000US-0215323P.
 PR 22-NOV-2000; 2000US-0252736P.
 PR 15-DEC-2000; 2000US-0255956P.
 PR 13-FEB-2001; 2001US-0268497P.
 PR 29-MAR-2001; 2001US-0279779P.
 PR 04-JUN-2001; 2001US-0295589P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Maillaird M, Hom C, Gailunas A, Jagodzinska B, Fang LY, John V;
 PI Freskos JN, Pulley SR, Beck JP, Tenbrink RE;
 XX WPI; 2002-171627/22.
 DR
 XX New substituted amines are e.g. amyloid beta peptide production
 PT

PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
 PT mild cognitive impairment and other degenerative diseases.

XX Example D; Page 344; 65lpp; English.

XX The present sequence is that of a peptide that incorporates the known
 CC cleavage site of beta-secretase on amyloid precursor protein (APP). The
 CC peptide, which may optionally be tagged with a fluorescent or chromogenic
 CC moiety, can be used in assays to determine the beta-secretase inhibitory
 CC activity of novel substituted amine compounds of the invention.
 CC Comparison of substrate cleavage results in the presence of an inhibitor
 CC and in the presence of a control provides a measure of the compound's
 CC inhibitory activity. Novel compounds of the invention are effective
 CC inhibitors of beta-secretase, inhibit beta-secretase mediated cleavage of
 CC APP, are effective inhibitors of A beta production, and/or effectively
 CC reduce amyloid beta deposits or plaques. They are used in the treatment
 CC or prevention of diseases characterised by amyloid deposits in the brain,
 CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
 CC prevent or delay the onset of AD, for treating mild cognitive impairment
 CC (MCI), preventing or delaying the onset of AD in those who would progress
 CC from MCI to AD, for treating Down's syndrome and hereditary cerebral
 CC haemorrhage with Amyloidosis of the Dutch type, for treating cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages, for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, and dementia associated with cortical
 CC basal degeneration, and for treating diffuse Lewy body type of AD (all
 CC claimed)

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |.:|:|
 Db 3 VNLDAAEF 9

RESULT 121

ABB77871
 ID ABB77871 standard; peptide; 9 AA.

XX ABB77871;

XX 27-SEP-2002 (first entry)

XX A beta-amyloid precursor protein (APP) inhibitor peptide.

XX Beta-amyloid precursor protein; APP; APP inhibitor peptide; BACE;
 KW beta site APP cleaving enzyme; protein coordinate data; APP751;
 KW Swedish family mutation; Alzheimer's disease.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 5 /label= Sta
 FT /note= "statine"

XX WO200225276-A1.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US029387.

XX 22-SEP-2000; 2000US-0234576P.

XX (AMHP) AMERICAN HOME PROD CORP.

PI Choppa R, Svenson K, Annis B, Akopian TN, Bard J, Stahl ML;
 PI Somers WS;
 XX WPI; 2002-519081/55.

XX Crystallized complex of beta-site amyloid precursor protein (APP)
 PT cleaving enzyme (BACE) and APP inhibitor peptide useful for identifying
 PT agents that interact with active site of BACE or active site of APP
 PT binding protein or peptide.

XX Claim 1; Page 22; 88pp; English.

XX The present sequence represents a beta-amyloid precursor protein (APP)
 CC inhibitor peptide. This peptide inhibits binding between APP and BACE
 CC (beta site APP cleaving enzyme). The specification describes a
 CC crystallized complex of BACE and the present APP inhibitor. Protein
 CC coordinate data for BACE is given in the specification. The APP inhibitor
 CC peptide is based on the P10 to P4' APP751 Swedish family mutation. The
 CC crystallized complex is used for identifying an agent that interacts with
 CC an active site of BACE or an active site of an APP binding protein or
 CC peptide. The agents are useful in the treatment and/or prevention of
 CC Alzheimer's disease

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 5; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |.:|:|
 Db 3 VNXXAAEF 9

RESULT 122

ABP97975

ID ABP97975 standard; peptide; 9 AA.

XX ABP97975;

XX 17-JUN-2003 (first entry)

XX Synthetic substrate comprising beta-secretase cleavage site.

XX Substrate; beta-secretase; alkylamide derivative; Alzheimer's disease;
 KW cognitive impairment; Down's syndrome; Hereditary Cerebral Haemorrhage;
 KW Parkinson's disease; cerebral amyloid angiopathy; degenerative dementia;
 KW supranuclear palsy; cortical basal degeneration.

XX Synthetic.

XX WO2003006423-A1.

XX 23-JAN-2003.

XX 11-JUL-2002; 2002WO-US022255.

XX 11-JUL-2001; 2001US-0304525P.

XX 30-JUL-2001; 2001US-0308756P.

XX 17-DEC-2001; 2001US-0341341P.

XX 17-DEC-2001; 2001US-0341416P.

XX 21-DEC-2001; 2001US-0344872P.

XX 21-DEC-2001; 2001US-0380574P.

XX (ELAN-) ELAN PHARM INC.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gailunas A, Hom R, John V, Maillard M, Chrusciel RA, Fisher J;

PI Jacobs J, Freskos JN, Brown DL, Fobian YM;

XX WPI; 2003-239223/23.

XX New N-(3-amino-2-hydroxypropyl) alkylamide derivatives are beta secretase

PT inhibitors used for treating e.g. Alzheimer's disease and Down's
 PT syndrome.
 XX
 PS Example D; Page 139; 205pp; English.
 XX
 CC The present sequence represents a synthetic substrate comprising a beta-
 CC secretase cleavage site. The substrate was used to assay beta-secretase
 CC activity in the presence or absence of inhibitory compounds of the
 CC invention. The invention describes N-(3-Amino-2-hydroxypropyl) alkylamide
 CC derivatives of a formula given in the specification. Compounds of the
 CC invention are used for treating or preventing Alzheimer's disease, mild
 CC cognitive impairment, Down's syndrome, Hereditary Cerebral Haemorrhage
 CC with Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy, other
 CC degenerative dementias and diffuse Lewy body type of Alzheimer's disease.
 CC They are also used for dementias of mixed vascular and degenerative
 CC origin, dementia associated with Parkinson's disease, dementia associated
 CC with progressive supranuclear palsy and dementia associated with cortical
 CC basal degeneration
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 [:::|]
 Db 3 VNLDAAEF 9

RESULT 123

ABP57515
 ID ABP57515 standard; peptide; 9 AA.

XX AC ABP57515;

XX DT 26-APR-2003 (first entry)

XX DE Differentially isotopically labelled (DiMas) peptide #8.

XX KW Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
 KW isotope; protease.

XX OS Synthetic.

XX PN WO2003001206-A1.

XX PD 03-JAN-2003.

XX PF 25-JUN-2002; 2002WO-GB002921.

XX PR 26-JUN-2001; 2001GB-00015581.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Mckewn SC;

XX DR WPI; 2003-184066/18.

PT Analyzing cleavage of polymer, by providing polymer sample, incubating
 PT the sample with labeled isotope for cleavage at potential cleavage site,
 PT and analyzing the masses of any uncleaved fragments by mass spectrometry.

XX Example 3; Page 25; 73pp; English.

XX CC The present invention describes a method (M1) for analysing cleavage of a
 CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
 CC of the polymer molecules having been labeled at a position on one side of
 CC the potential cleavage site with a first isotopic label and a portion of
 CC the polymer molecules having been labeled at a position on the opposite
 CC side of the potential cleavage site with a second isotopic label; (b)
 CC incubating the sample under conditions suitable for cleavage at the
 CC potential cleavage site; and (c) analysing the mass(es) of any cleaved

CC fragments by mass spectrometry and thereby determining whether and/or
 CC where cleavage has taken place. M1 is useful for analysing cleavage of a
 CC polymer, where the polymer is a linear polymer, and comprises a peptide
 CC or protein. Methods from the present invention can be used in discovering
 CC new or improved synthetic substrates for both known and unknown enzymes,
 CC e.g. enzymes identified from the human genome. The methods are also
 CC useful to identify the sequence origin, and in screening methods to
 CC identify new substrates for enzymes, in positional peptide scanning
 CC libraries, in vivo/ex vivo/in vitro peptide, and in assaying methods
 CC for oligonucleotide or peptide sequencing and in measuring differential
 CC protein expression. The methods are useful for monitoring the cleavage of
 CC polypeptides or polynucleotides, and for determining optimal polymer
 CC substrates. ABP57505 to ABP57605 represent peptides used in the
 CC exemplification of the present invention

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 [:::|]
 Db 3 VNLDAAEF 9

RESULT 124

ABP57084

ID ABP57084 standard; peptide; 9 AA.

XX AC ABP57084;

XX DT 14-APR-2003 (first entry)

XX DE Synthetic oligopeptide substrate SEQ ID NO:8.

XX KW Beta-hydroxyamine derivative; nootropic; neuroprotective; MCI;
 KW Alzheimer's disease; mild cognitive impairment; Down's syndrome;
 KW hereditary cerebral haemorrhage; amyloidosis; lobar haemorrhage;
 KW cerebral amyloid angiopathy; degenerative dementia; dementia;
 KW Parkinson's disease; progressive supranuclear palsy; APP;
 KW cortical basal degeneration; amyloid precursor protein; substrate.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "biotinylated"
 XX PN WO2003002122-A1.

XX PD 09-JAN-2003.

XX PF 27-JUN-2002; 2002WO-US020754.

XX PR 27-JUN-2001; 2001US-0301210P.

XX PR 18-SEP-2001; 2001US-0323396P.

XX PR 19-NOV-2001; 2001US-0332736P.

XX PA (ELAN-) ELAN PHARM INC.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI John V, Hom R, Tucker J;

XX DR WPI; 2003-201464/19.

XX PT New beta-hydroxyamine derivatives are beta secretase inhibitors used for
 PT treating e.g. Alzheimer's disease, Down's syndrome and cerebral amyloid
 PT angiopathy.

XX PS Example D; Page 56; 96pp; English.

XX CC The present invention describes beta-hydroxyamine derivatives (I). Also

CC described is a method for the preparation of (I). (I) has neurotropic and
 CC neuroprotective activities. (I) can be used as an inhibitor of: beta-
 CC secretase activity; beta amyloid peptide (A beta) production; beta
 CC deposition; and amyloid precursor protein (APP) cleavage. (I) can be used
 CC for preventing or delaying the onset of Alzheimer's disease, for treating
 CC mild cognitive impairment (MCI), Down's syndrome, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch-type and cerebral amyloid
 CC angioathy and preventing its potential consequences i.e. single and
 CC recurrent lobar haemorrhages, for treating other degenerative dementias
 CC (including dementias of mixed vascular and degenerative origin, dementia
 CC associated with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration)
 CC or diffuse Lewy body type of Alzheimer's disease. The present sequence
 CC represents a synthetic oligopeptide substrate, which is used in the
 CC exemplification of the present invention

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 125

ABP71468
 ID ABP71468 standard; peptide; 9 AA.

AC ABP71468;

DT 15-MAY-2003 (first entry)

XX Beta-secretase cleavage site comprising oligopeptide.

XX APP; alpha-hydroxyamide statine; neurotropic; neuroprotective; haemostatic;
 KW beta-secretase; beta Amyloid; A beta; amyloid precursor protein;
 KW degenerative dementia; Alzheimer's disease; Down's syndrome;
 KW Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type;
 KW cerebral amyloid angiopathy.

XX Synthetic.

PH Key Location/Qualifiers
 FT Cleavage-site 5..6 /note= "beta-secretase cleavage site"

XX WO2003006021-A1.

XX 23-JAN-2003.

XX 10-JUL-2002; 2002WO-US021742.

XX 10-JUL-2001; 2001US-0304128P.

PR 05-OCT-2001; 2001US-0327424P.

XX (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

PA (SCHO/) SCHOSTAREZ H J.

PA (CHRU/) CHRUSCIEL R A.

XX Schostarez HJ, Chrusciel RA;

XX WPI; 2003-267942/26.

XX New alpha-hydroxyamide statine derivatives useful for the treatment of
 PT e.g. Alzheimer's disease.

XX Example D; Page 97; 142pp; English.

XX The invention relates to alpha-hydroxyamide statine derivatives of

CC specified formula. The compounds are capable of slowing beta amyloid
 CC peptide (A beta) formation and/or deposition in the brain and are
 CC effective inhibitors of beta-secretase. They inhibit beta-secretase-
 CC mediated cleavage of APP and are effective inhibitors of A beta
 CC production to reduce amyloid beta deposit or plaques. The compounds are
 CC useful in the manufacture of a medicament for treating or preventing e.g.
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type,
 CC cerebral amyloid angiopathy, other degenerative dementias (including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration)
 CC or diffuse Lewy body type of Alzheimer's disease in a patient. The
 CC present sequence represents an oligopeptide that incorporates the known
 CC beta-secretase cleavage site, used in assays for beta-secretase
 CC inhibition by the inhibitory compounds of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 126

AAO16449
 ID AAO16449 standard; peptide; 9 AA.

XX AAO16449;

DT 10-APR-2003 (first entry)

XX Beta-secretase synthetic APP substrate peptide, SEQ ID No 8.

XX Alzheimer's disease; bicyclo compound; amyloid beta peptide;
 KW beta-amyloid plaque; cognitive activity; amyloid precursor protein; APP;
 KW degenerative dementia; Parkinson's disease; cerebral amyloid angiopathy;
 KW beta-secretase; substrate.

XX Synthetic.

PH Key Location/Qualifiers
 FT Modified-site 1 /note= "Labelled with biotin"
 FT Cleavage-site 5..6 /note= "Cleaved between these two residues by beta-
 FT secretase"

XX WO2003000261-A1.

XX 03-JAN-2003.

XX 25-JUN-2002; 2002WO-US020054.

XX 25-JUN-2001; 2001US-0300671P.

XX (ELAN-) ELAN PHARM INC.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX Beck JP;

XX WPI; 2003-201375/19.

XX Treatment or prevention of Alzheimer's disease involves use of bicyclo
 PT compounds.

XX Example D; Page 60; 116pp; English.

XX The invention comprises a method for the treatment or prevention of

CC Alzheimer's disease. The method involves the administration of bicyclo
 CC compounds or their salts. A major factor in the development of
 CC Alzheimer's disease is the deposition of amyloid beta peptide (beta-
 CC amyloid plaques) in areas of the brain responsible for cognitive
 CC activities. Amyloid beta protein is derived by proteolysis (by
 CC secretases) of the amyloid precursor protein (APP). The method of the
 CC invention is useful for treating and delaying the onset of Alzheimer's
 CC disease. The method is also useful for the treatment of other
 CC degenerative dementias (e.g. Parkinson's disease and cerebral amyloid
 CC angiopathy). The method of the invention is useful for inhibiting beta-
 CC secretase activity - thereby inhibiting cleavage of an APP and inhibiting
 CC production of amyloid beta peptide. The present amino acid sequence
 CC represents a synthetic APP substrate for beta-secretase
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 Db 3 VNLDAAEF 9
 |:::|

RESULT 127
 ABR711269
 ID ABR711269 standard; peptide; 9 AA.
 AC ABR711269;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE Oligopeptide substrate used for beta-secretase assay.

XX APP; aminediol; amyloid precursor protein; beta amyloid; A-beta;
 KW beta-secretase; neurotropic; neuroprotective; antiparkinsonian;
 KW cerebroprotective; haemostatic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal biotinylation"
 FT Cleavage-site 5..6
 FT /note= "cleavage site for beta-secretase"
 XX
 PN WO2003006453-A1.
 XX
 PD 23-JAN-2003.

XX 10-JUL-2002; 2002WO-US021709.
 XX
 PR 10-JUL-2001; 2001US-0304129P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Schostarez HJ, Chrusciel RA;
 PI WPI; 2003-210414/20.
 XX
 DR
 XX New aminediols are beta-secretase inhibitors, useful for the treatment of
 PT e.g. Alzheimer's disease, cognitive impairment, Down's syndrome, and
 PT degenerative dementias.
 XX
 PS Example D; Page 145; 190pp; English.

XX The invention relates to aminediol derivatives of specified formula. The
 CC compounds are capable of slowing beta amyloid (A-beta) peptide formation
 CC and/or deposition in the brain. They are effective inhibitors of beta-
 CC secretase and inhibit beta-secretase-mediated cleavage of amyloid
 CC precursor protein (APP). Thus they effectively inhibit A-beta production

CC and helps to reduce amyloid beta deposit or plaques. The compounds are
 CC useful in the manufacture of a medicament for treating or preventing
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-Type,
 CC cerebral amyloid angiopathy, other degenerative dementias (including
 CC dementias of mixed vascular and degenerative origin, dementia associated
 CC with Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, dementia associated with cortical basal degeneration)
 CC or diffuse Lewy body type of Alzheimer's disease in a patient especially
 CC human. Sequences ABR71269-270 represent oligopeptide substrates
 CC containing known beta-secretase cleavage site are used to assay beta-
 CC secretase activity
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 Db 3 VNLDAAEF 9
 |:::|

RESULT 128
 ABR44377
 ID ABR44377 standard; peptide; 9 AA.

AC ABR44377;
 XX
 DT 14-JUL-2003 (first entry)
 XX

DE Oligopeptide #1 incorporating cleavage site of beta-secretase.

XX Neurotropic; neuroprotective; hemostatic; Alzheimer's disease;
 KW Down's syndrome; Hereditary Cerebral Hemorrhage; beta-secretase.
 XX
 OS Synthetic.

XX WO2003027068-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-US030231.
 XX
 PR 24-SEP-2001; 2001US-0324407P.
 XX
 XX (ELAN-) ELAN PHARM INC.

XX Gailunas A, Tucker JA, John V;
 PI WPI; 2003-421148/39.
 XX

XX New substituted amines useful for the treatment of e.g. Alzheimer's
 PT disease, mild cognitive impairment and down's syndrome.
 PT

PS Example D; Page 106; 140pp; English.

XX This invention relates to substituted amines that are considered
 CC neurotropic, neuroprotective and hemostatic in their action. They are
 CC useful in the manufacture of a medicament for treating or preventing
 CC Alzheimer's disease, mild cognitive impairment, Down's syndrome,
 CC Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type and
 CC other degenerative dementias. The compounds are capable of slowing A-beta
 CC peptide formation and deposition in the brain and are effective
 CC inhibitors of beta-secretase that inhibit beta-secretase-mediated
 CC cleavage of APP that are effective inhibitors of A beta production and
 CC effective to reduce amyloid beta deposit or plaques. The present sequence
 CC represents a synthetic oligopeptide that incorporates the cleavage site of
 CC beta-secretase
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 129
 ABP58375
 ID ABP58375 standard; peptide; 9 AA.
 XX
 AC ABP58375;
 XX
 DT 07-APR-2003 (first entry)
 XX
 DE Beta-secretase amyloid precursor protein substrate.
 XX
 KW Beta-secretase; substrate; amyloid precursor protein; inhibitor;
 KW hydroxyl alkyl amine; Alzheimer's disease; neurotropic; neuroprotective;
 KW haemostatic; antiparkinsonian.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH Cleavage-site 5..6
 FT
 XX
 XX WO200298849-A2.
 PN
 XX
 PD 12-DEC-2002.
 XX
 XX 31-MAY-2002; 2002WO-US017698.
 XX
 PR 01-JUN-2001; 2001US-0295332P.
 PR 19-NOV-2001; 2001US-0332639P.
 PR 28-DEC-2001; 2001US-0343772P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PA
 XX
 PI Freskos J, Aquino J, Brown DL, Fang L, Fobian YM, Gailunas A;
 PI Guinn A, Varghese J, Romero AG, Tucker J, Tung J, Walker D;
 XX
 XX WPI; 2003-201287/19.
 XX
 PT New hydroxy alkyl amine compounds are beta-secretase activity inhibitors
 PT useful for treatment of e.g. Alzheimer's disease, mild cognitive
 PT impairment, Down's syndrome, hereditary cerebral hemorrhage.
 XX
 XX Example D; Page 197; 360pp; English.
 XX
 CC The present sequence is an example of a synthetic amyloid precursor
 CC protein (APP) substrate that includes a beta-secretase cleavage site.
 CC Cleavage products can be detected using HPLC, or fluorogenic or
 CC chromogenic detection methods. The invention provides novel hydroxy alkyl
 CC amine compounds that have beta-secretase inhibitor activity. Beta-
 CC secretase cleaves APP to amyloid beta peptide, found in the brains of
 CC Alzheimer's disease patients. The novel compounds halt or reduce A-beta
 CC production from APP and reduce or eliminate the formation of beta-amyloid
 CC deposits in the brain. They are useful for the manufacture of a
 CC medicament for the treatment or prevention of Alzheimer's disease, mild
 CC cognitive impairment, Down's syndrome, hereditary cerebral hemorrhage
 CC with amyloidosis of the Dutch type, cerebral amyloid angiopathy, other
 CC degenerative dementias, dementias of mixed vascular and degenerative
 CC origin, dementia associated with Parkinson's disease, dementia associated
 CC with progressive supranuclear palsy, dementia associated with cortical
 CC basal degeneration, diffuse Lewy body type of Alzheimer's disease (all
 CC claimed) and for treating frontotemporal dementias with parkinsonism

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;

Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 130
 AAO26801
 ID AAO26801 standard; peptide; 9 AA.
 XX
 AC AAO26801;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Beta-secretase substrate peptide, SEQ ID No 8.
 XX
 KW Neurotropic; neuroprotective; haemostatic; antiparkinsonian; aminoalcohol;
 KW Alzheimer's disease; mild cognitive impairment; MCI; Down's syndrome;
 KW Hereditary Cerebral Haemorrhage; Amyloidosis; Dutch-Type;
 KW cerebral amyloid angiopathy; single; recurrent lobar haemorrhages;
 KW degenerative dementia; Parkinson's disease; cortical basal degeneration;
 KW progressive supranuclear palsy; Lewy body type; beta-secretase; enzyme;
 KW substrate.
 XX
 OS Unidentified.
 XX
 XX WO2002100820-A1.
 PN
 XX 19-DEC-2002.
 XX
 XX 11-JUN-2002; 2002WO-US019067.
 XX
 PR 11-JUN-2001; 2001US-0297420P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PA
 XX
 PI Maillard M, Tucker JA;
 PI
 XX
 DR WPI; 2003-167387/16.
 XX
 XX New substituted aminoalcohols useful for the treatment of e.g.
 PT Alzheimer's disease, mild cognitive impairment, Down's syndrome or
 PT dementia associated with Parkinson's disease.
 XX
 XX Example D; Page 119; 206pp; English.
 XX
 CC The invention relates to novel substituted aminoalcohols, their esters
 CC and salts. The novel substituted aminoalcohols can be used for treating a
 CC patient who has, or in preventing a patient from getting, a disease or
 CC condition (e.g. Alzheimer's disease), for helping prevent or delay the
 CC onset of the Alzheimer's disease, for treating patients with mild
 CC cognitive impairment (MCI) and preventing or delaying the onset of
 CC Alzheimer's disease in those who would progress from MCI to Alzheimer's
 CC disease, for treating Down's syndrome, for treating humans who have
 CC hereditary cerebral haemorrhage with amyloidosis of the Dutch-type, for
 CC treating cerebral amyloid angiopathy and preventing its potential
 CC consequences i.e. single and recurrent lobar haemorrhages, for treating
 CC other degenerative dementias (including dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration) or diffuse Lewy body type of
 CC Alzheimer's disease. This sequence represents a peptide substrate of beta
 CC -secretase used in an enzyme inhibition assay for analysing the
 CC inhibitory activity of the novel compounds of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;

Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 VXXXAEF 7
Db      3 VNLDADF 9

RESULT 131
ABG75940
ID      ABG75940 standard; peptide; 9 AA.
XX
AC      ABG75940;
XX
DT      07-MAY-2003 (first entry)
XX
DE      Synthetic Amyloid precursor protein (APP) substrate #6.
XX
KW      Amyloid precursor protein; APP; substituted cyclic amide;
KW      Alzheimer's disease; mild cognitive impairment; MCI; Down's syndrome;
KW      hereditary cerebral haemorrhage with Amyloidosis of the dutch type;
KW      cerebral amyloid angiopathy; degenerative dementia; dementia;
KW      diffuse Lewy body type of Alzheimer's disease; Parkinson's disease;
KW      progressive supranuclear palsy; cortical basal degeneration;
KW      beta-secretase inhibitor.
XX
OS      Synthetic.
XX
PN      WO2002100856-A1.
XX
PD      19-DEC-2002.
XX
PF      12-JUN-2002; 2002WO-US019076.
XX
PR      12-JUN-2001; 2001US-0297546P.
PR      19-NOV-2001; 2001US-0333083P.
XX
PA      (ELAN-) ELAN PHARM INC.
PA      (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI      Pulley SR, Beck JP, Tenbrink RE;
XX
WPI; 2003-278223/27.
XX
PT      New substituted cyclic amides useful as beta-secretase and amyloid
PT      precursor protein inhibitors for treating e.g. Alzheimer's disease and
PT      Down's syndrome.
XX
PS      Example D; Page 113; 164pp; English.
XX
CC      The invention describes substituted cyclic amides (I). (I) are useful in
CC      the manufacture of a medicament for treating, preventing and delaying
CC      Alzheimer's disease, for treating mild cognitive impairment (MCI), Down's
CC      syndrome, hereditary cerebral haemorrhage with Amyloidosis of the dutch
CC      type, cerebral amyloid angiopathy, other degenerative dementias and
CC      diffuse Lewy body type of Alzheimer's disease. (I) is also useful for
CC      treating dementia associated with Parkinson's disease, progressive
CC      supranuclear palsy and cortical basal degeneration. The compounds are
CC      capable of slowing A-beta peptide formation and/or deposition in the
CC      brain and are effective inhibitors of beta-secretase, that inhibit beta-
CC      secretase-mediated cleavage of APP, that are effective inhibitors of A
CC      beta production and/or effective to reduce amyloid beta deposit or
CC      plaques. This is the amino acid sequence of an amyloid precursor protein
CC      (APP) substrate that can be cleaved by beta-secretase and is therefore
CC      used to assay beta-secretase activity in the presence and absence of the
CC      inhibitory compounds of the invention
XX
SQ      Sequence 9 AA;

Query Match      100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
Db      3 VNLDADF 9

```

```

Db      3 VNLDADF 9

RESULT 132
ABP71630
ID      ABP71630 standard; peptide; 9 AA.
XX
AC      ABP71630;
XX
DT      29-MAY-2003 (first entry)
XX
DE      Beta-secretase activity assaying oligopeptide substrate.
XX
KW      APP; diaminediol; A-beta; beta-secretase; amyloid precursor protein;
KW      beta amyloid; nootropic; neuroprotective; antiparkinsonian; haemostatic.
XX
OS      Synthetic.
XX
PH      Key      Location/Qualifiers
FT      Modified-site 1
FT      Cleavage-site 5..6
FT      /note= "N-terminal biotin"
FT      /note= "beta-secretase cleavage site"
XX
PN      WO2003006013-A1.
XX
PD      23-JAN-2003.
XX
PF      10-JUL-2002; 2002WO-US022459.
XX
PR      10-JUL-2001; 2001US-0304305P.
PR      30-NOV-2001; 2001US-0334480P.
XX
PA      (ELAN-) ELAN PHARM INC.
PA      (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI      Schostarez HJ, Chrusciel RA;
XX
WPI; 2003-289727/28.
XX
PT      New diaminediols useful for the treatment of e.g. Alzheimer's disease.
XX
PS      Example D; Page 139; 182pp; English.
XX
CC      The invention relates to diaminediol derivatives of specified formula.
CC      The compounds are capable of slowing A-beta peptide formation and/or
CC      deposition in the brain and are effective inhibitors of beta-secretase.
CC      They can inhibit beta-secretase-mediated cleavage of APP (amyloid
CC      precursor protein) and are effective inhibitors of A beta production and/
CC      or effective to reduce amyloid beta deposit or plaques. The compounds are
CC      useful in the manufacture of a medicament for treating or preventing e.g.
CC      Alzheimer's disease, mild cognitive impairment, Down's syndrome,
CC      Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type,
CC      cerebral amyloid angiopathy, other degenerative dementias (including
CC      dementias of mixed vascular and degenerative origin, dementia associated
CC      with Parkinson's disease, dementia associated with progressive
CC      supranuclear palsy, dementia associated with cortical basal degeneration)
CC      or diffuse Lewy body type of Alzheimer's disease in a patient e.g. human.
CC      Sequences ABP71630-631 represent synthetic APP oligopeptide substrates
CC      containing the known beta-secretase cleavage site and are used to assay
CC      beta-secretase activity
XX
SQ      Sequence 9 AA;

Query Match      100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
Db      3 VNLDADF 9

```

```

RESULT 133
AAE36000
ID AAE36000 standard; peptide; 9 AA.
XX
AC AAE36000;
XX
DT 26-JUN-2003 (first entry)
XX
DE APP substrate #6 used in the exemplification of the invention.
XX
KW Aminediol compound; beta secretase inhibitor; Alzheimer's disease; AD;
KW Hereditary Cerebral Haemorrhage with Amyloidosis of Dutch-Type; HCHWA-D;
KW cognitive impairment; cerebral amyloid angiopathy; Down's syndrome; APP;
KW amyloidosis; cortical basal degeneration; Parkinson's disease; therapy;
KW dementia; supranuclear palsy; amyloid precursor protein.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5..6
XX WO2002100818-A2.
XX
PD 19-DEC-2002.
XX
PF 13-JUN-2002; 2002WO-US018845.
XX
PR 13-JUN-2001; 2001US-0297827P.
XX
PR 19-NOV-2001; 2001US-0333084P.
XX
XX
PA (ELAN-) ELAN PHARM INC.
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Schostarez HJ, Chrusciel RA;
XX
DR WPI; 2003-201321/19.
XX
XX
XX New aminediol compounds are beta secretase inhibitors used for treating
XX e.g. Alzheimer's disease and dementia associated with Alzheimer's
XX disease.
XX
XX Example C; Page 160; 213pp; English.
XX
XX The invention relates to aminediol compounds including beta secretase
XX inhibitors, used for treating and preventing Alzheimer's disease (AD),
XX mild cognitive impairment, Down's syndrome, Hereditary Cerebral
XX Haemorrhage with Amyloidosis of Dutch-Type (HCHWA-D), cerebral amyloid
XX angiopathy, other degenerative dementias, dementias of mixed vascular and
XX degenerative origin, dementia associated with Parkinson's disease,
XX dementia associated with progressive supranuclear palsy, dementia
XX associated with cortical basal degeneration and diffuse Lewy body type of
XX Alzheimer's disease. The present sequence is APP (amyloid precursor
XX protein) substrate used in the exemplification of the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9
|:::|
|:::|

RESULT 134
ABR82372
ID ABR82372 standard; peptide; 9 AA.
XX
AC ABR82372;
XX
DT 06-NOV-2003 (first entry)
XX
XX

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```

DE Beta-secretase cleavage site containing oligopeptide substrate.
XX
KW APP; amino carboxamide; nootropic; neuroprotective; haemostatic;
KW antiparkinsonian; beta-secretase; amyloid precursor protein.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal biotinylation"
FT Cleavage-site 5..6 /note= "beta-secretase cleavage site"
XX WO2003057721-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000326.
XX
PR 04-JAN-2002; 2002US-0345316P.
PR 18-JAN-2002; 2002US-0350419P.
XX
XX (ELAN-) ELAN PHARM INC.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Jagodzinska B, Warpehowski MA;
XX WPI; 2003-645986/61.
XX
XX New substituted amino carboxamide compounds are beta secretase inhibitors
XX used for treating e.g. Alzheimer's disease and mild cognitive impairment
XX and Down's syndrome.
XX
XX Example D; Page 101; 133pp; English.
XX
XX The invention relates to substituted amino carboxamide compounds of
XX specified formula. The compounds can inhibit the activity beta-secretase
XX and can also inhibit amyloid precursor protein (APP) cleavage. They can
XX be used for treatment or prevention of Alzheimer's disease, mild
XX cognitive impairment, Down's syndrome, hereditary cerebral haemorrhage
XX with amyloidosis of the Dutch-type, cerebral amyloid angiopathy, other
XX degenerative dementias, dementias of mixed vascular and degenerative
XX origin, dementia associated with Parkinson's disease, dementia associated
XX with progressive supranuclear palsy, dementia associated with cortical
XX basal degeneration, or diffuse Lewy body type of Alzheimer's disease. The
XX present sequence represents a synthetic oligopeptide substrate containing
XX the known cleavage site of beta-secretase cleavage site
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9
|:::|
|:::|

RESULT 135
ABR56258
ID ABR56258 standard; peptide; 9 AA.
XX
AC ABR56258;
XX
DT 20-NOV-2003 (first entry)
XX
DE Amyloid Precursor Protein substrate #6.
XX
XX APP; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;
KW beta-secretase; Amyloid Precursor Protein.
XX
OS Synthetic.

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```

XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "Biotin-Ser"
XX FT Cleavage-site 5. .6
XX PN WO2003043618-A2.
XX PD
XX PF 30-MAY-2003.
XX PF 19-NOV-2002; 2002WO-US037180.
XX PR 19-NOV-2001; 2001US-0332863P.
XX PA (ELAN-) ELAN PHARM INC.
XX PA (PHAA ) PHARMACIA & UPJOHN.
XX PI Schostarez HJ, Hanson GJ;
XX XX WPI; 2003-532662/50.
XX XX
XX XX Treatment of Alzheimer's disease involves the use of amine diols or their
XX FT salts.
XX PS Example D; Page 227; 270pp; English.
XX XX
XX CC The present invention relates to novel amine diols and their salts, which
XX CC can be used for the treatment of Alzheimer's disease. The compounds are
XX CC inhibitors of beta-secretase, which cleaves Amyloid Precursor Protein
XX CC (APP) to produce A beta peptide, a major component of the amyloid plaques
XX CC found in the brains of Alzheimer's sufferers. APP substrates (ABR56251-
XX CC ABR56259) that can be cleaved by beta-secretase, were used to assay beta-
XX CC secretase activity in the presence or absence of the compounds of the
XX CC invention
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
3 VNLDAEF 9

RESULT 136
ABR62018
ID ABR62018 standard; peptide; 9 AA.
XX AC ABR62018;
XX DT 03-OCT-2003 (first entry)
XX DE Beta-secretase cleavage site containing oligopeptide substrate.
XX XX APP; Alzheimer's disease; neurotropic; neuroprotective; cerebroprotective;
XX KW beta amyloid peptide; amyloid precursor protein; beta-secretase; A beta;
XX KW haemostatic.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal biotinylation"
XX FT Cleavage-site 5. .6
XX XX WO2003047576-A1.
XX PN
XX PD 12-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US040038.
XX XX

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PR 04-DEC-2001; 2001US-0335666P.
XX XX (ELAN-) ELAN PHARM INC.
XX XX Varghese J;
XX XX WPI; 2003-558913/52.
XX XX
XX XX Treating Alzheimer's disease, mild cognitive impairment and other similar
XX PT diseases comprises administering beta secretase inhibiting heterocyclic
XX PT compounds.
XX PS Example D; Page 65; 149pp; English.
XX XX
XX CC The invention relates to treating or preventing Alzheimer's disease and
XX CC related diseases and involves administering heterocyclic compounds of
XX CC specified formula. The compounds can inhibit the activity of beta-
XX CC secretase. It can also inhibit the production and/or deposition of beta
XX CC amyloid peptide (A beta) in the brain and inhibit beta-secretase mediated
XX CC cleavage of amyloid precursor protein (APP). The compounds can be used
XX CC for treating, preventing or delaying the onset of Alzheimer's disease,
XX CC for treating mild cognitive impairment (MCI) and preventing or delaying
XX CC the onset of Alzheimer's disease in those with MCI, for treating Down's
XX CC syndrome, hereditary cerebral haemorrhage with amyloidosis of the Dutch-
XX CC type, cerebral amyloid angiopathy and preventing its potential
XX CC consequences i.e. single and recurrent lobar haemorrhages, other
XX CC degenerative dementias (including dementias of mixed vascular and
XX CC degenerative origin, dementia associated with Parkinson's disease,
XX CC dementia associated with progressive supranuclear palsy, dementia
XX CC associated with cortical basal degeneration) or diffuse Lewy body type of
XX CC Alzheimer's disease. The present sequence represents a synthetic
XX CC oligopeptide substrate containing the known cleavage site of beta-
XX CC secretase, used to assay beta-secretase activity
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
3 VNLDAEF 9

RESULT 137
ABR61887
ID ABR61887 standard; peptide; 9 AA.
XX AC ABR61887;
XX DT 12-SEP-2003 (first entry)
XX DE Beta-secretase cleavage site containing oligopeptide substrate.
XX XX APP; Alzheimer's disease; beta-secretase; beta amyloid peptide; A beta;
XX KW amyloid precursor protein; neurotropic; neuroprotective.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal biotin"
XX FT Cleavage-site 5. .6
XX FT /note= "beta-secretase cleavage site"
XX XX WO2003045378-A1.
XX PN
XX PD 05-JUN-2003.
XX PF 21-NOV-2002; 2002WO-US037360.
XX PF 21-NOV-2001; 2001US-0334692P.
XX PR

```

XX PA (ELAN-) ELAN PHARM INC.
 XX PA (PHAA) PHARMACIA & UPJOHN CO.
 XX PI John V;
 XX DR WPI; 2003-577200/54.
 XX
 XX Use of amino acid derivatives for e.g. treating mild cognitive impairment
 PT and treating, preventing or delaying the onset of the Alzheimer's
 PT disease.
 XX
 XX Example D; Page 53; 204pp; English.
 XX
 XX The invention relates to the treatment of Alzheimer's disease (AD) and
 CC involves administration of amino acid derivatives of specified formula.
 CC The derivatives act as inhibitors of beta-secretase and inhibits the
 CC production and deposition of beta Amyloid peptide (A beta). They also
 CC inhibit the cleavage of amyloid precursor protein (APP). The derivatives
 CC can be used for treating, preventing or delaying the onset of AD, for
 CC treating mild cognitive impairment (MCI) and preventing or delaying the
 CC onset of AD in those who would progress from MCI to AD; treating Down's
 CC syndrome, hereditary cerebral haemorrhage with amyloidosis of the Dutch-
 CC type, cerebral amyloid angiopathy and preventing its potential
 CC consequences i.e. single and recurrent lobar haemorrhages, other
 CC degenerative dementias (including dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration) or diffuse Lewy body type of
 CC Alzheimer's disease. The present sequence represents a synthetic
 CC oligopeptide substrate containing the known beta-secretase cleavage site,
 CC used to assay beta-secretase activity
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 7; DB 6; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 Db |:::|
 3 VNLDAAEF 9
 RESULT 138
 ABR56195
 ID ABR56195 standard; peptide; 9 AA.
 AC ABR56195;
 XX 18-DEC-2003 (first entry)
 XX Amyloid precursor protein, APP, substrate #7.
 XX APP; nootropic; neuroprotective; cerebroprotective; haemostatic;
 KW Alzheimer's disease; beta-secretase; Amyloid Precursor Protein; APP;
 KW degenerative dementia.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal Biotin"
 FT Cleavage-site 5. .6
 FT
 XX WO2003037325-A1.
 PN
 XX 08-MAY-2003.
 XX
 XX 29-OCT-2002; 2002WO-US034678.
 XX
 XX 29-OCT-2001; 2001US-0351152P.
 XX
 XX

PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Beck JP;
 XX WPI; 2003-482086/45.
 XX
 XX Treating e.g. Alzheimer's disease, mild cognitive impairment, Down's
 PT syndrome and cerebral amyloid angiopathy comprises administering hydroxy
 PT substituted amide compounds.
 XX
 XX Example D; Page 67; 90pp; English.
 XX
 XX The present invention relates to a method for treating or preventing
 CC Alzheimer's disease. The method comprises administering hydroxy
 CC substituted amide compounds. The compounds inhibit beta-secretase, which
 CC cleaves Amyloid Precursor Protein (APP) to produce A beta protein, a
 CC major component of the amyloid plaques found in the brains of Alzheimer's
 CC sufferers. The method is also useful for treating mild cognitive
 CC impairment, Down's disease, hereditary cerebral haemorrhage with
 CC amyloidosis of the Dutch-type, cerebral amyloid angiopathy and other
 CC degenerative dementias. The present sequence is a synthetic APP substrate
 CC which can be cleaved by beta-secretase. This peptide was used to assay
 CC beta-secretase activity in the presence or absence of the inhibitory
 CC compounds of the invention
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 7; DB 7; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXXAEEF 7
 Db |:::|
 3 VNLDAAEF 9
 RESULT 139
 ADC29723
 ID ADC29723 standard; peptide; 9 AA.
 XX ADC29723;
 AC
 XX 18-DEC-2003 (first entry)
 XX Synthetic beta-secretase oligopeptide substrate #1.
 XX N,N'-Substituted-1,3-diamino-2-hydroxypropane derivative;
 KW Alzheimer's disease; Down's syndrome; hereditary cerebral haemorrhage;
 KW Dutch-Type amyloidosis; cerebral angiopathy; degenerative dementia;
 KW Parkinson's disease; progressive supranuclear palsy;
 KW cortical basal degeneration; beta-secretase; amyloid precursor protein;
 KW APP; substrate.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 5. .6 /note= "Beta-secretase cleavage site"
 FT
 FT
 XX WO2003040096-A2.
 PN
 XX 15-MAY-2003.
 XX
 XX 08-NOV-2002; 2002WO-US036072.
 XX
 XX 08-NOV-2001; 2001US-0337122P.
 PR 28-DEC-2001; 2001US-0344086P.
 PR 03-JAN-2002; 2002US-0345635P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX

PI John V, Maillard M, Jagodzinska B, Beck JP, Gailunas A, Fang L;
 PI Sealy J, Tenbrink R, Freskos J, Mickelson J, Samala L, Hom R;
 XX WPI; 2003-505059/47.
 XX
 XX New N,N'-substituted-1,3-diamino-2-hydroxypropane derivatives are beta
 PT secretase inhibitors used for treating e.g. Alzheimer's disease, Down's
 PT syndrome and hereditary cerebral hemorrhage.
 XX
 XX Example D; SEQ ID NO 8; 1243pp; English.

PS
 XX The invention comprises N,N'-Substituted-1,3-diamino-2-hydroxypropane
 CC derivatives. The compounds of the invention are useful for treating:
 CC Alzheimer's disease, Down's syndrome, hereditary cerebral haemorrhage
 CC with amyloidosis of the Dutch-type, cerebral angiodopathy, degenerative
 CC dementia, Parkinson's disease, progressive supranuclear palsy and
 CC cortical basal degeneration, and diffuse Lewy body of Alzheimer's
 CC disease. The compounds of the invention also inhibit beta-secretase
 CC mediated cleavage of amyloid precursor protein (APP). The present amino
 CC acid sequence represents a synthetic oligopeptide substrate that can be
 CC cleaved by beta-secretase.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 7; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 DB 3 VNLDAEF 9

RESULT 140

ADC26557
 ID ADC26557 standard; peptide; 9 AA.

XX AC ADC26557;

XX DT 18-DEC-2003 (first entry)

XX DE Beta-secretase cleavage site peptide SEQ ID 4.

XX KW nontropic; neuroprotective; Alzheimer's disease;

XX KW beta-secretase cleavage site.

XX OS Unidentified.

XX FN WO2003065012-A2.

XX XX 07-AUG-2003.

XX PF 03-FEB-2003; 2003WO-US003236.

XX PR 01-FEB-2002; 2002US-00066319.

XX (UNMI) UNIV MICHIGAN.

XX PI Ross BD, Rehemtulla A;

XX DR WPI; 2003-663499/62.

XX The invention relates to a novel chimeric nucleic acid encoding a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a

XX Claim 15; SEQ ID NO 4; 41pp; English.

XX The invention relates to a novel chimeric nucleic acid encoding a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a

CC protease cleavage site and the third domain comprises a reporter molecule
 CC and where the protease cleavage site is between the Golgi retention
 CC signal peptide and the reporter molecule. The molecules of the invention
 CC demonstrate nontropic and neuroprotective activities and may be useful
 CC for detecting and measuring protease activity or for identifying
 CC modulators of protease activity in order to detect, prevent or ameliorate
 CC Alzheimer's disease. The current sequence is that of the beta-secretase
 CC cleavage site peptide SEQ ID 4 of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 7; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 DB 3 VNLDAEF 9

RESULT 141

ADC26556

ID ADC26556 standard; peptide; 9 AA.

XX AC ADC26556;

XX DT 18-DEC-2003 (first entry)

XX DE Beta-secretase cleavage site peptide SEQ ID 3.

XX KW nontropic; neuroprotective; Alzheimer's disease;

XX KW beta-secretase cleavage site.

XX OS Unidentified.

XX PN WO2003065012-A2.

XX XX 07-AUG-2003.

XX PF 03-FEB-2003; 2003WO-US003236.

XX PR 01-FEB-2002; 2002US-00066319.

XX (UNMI) UNIV MICHIGAN.

XX PI Ross BD, Rehemtulla A;

XX DR WPI; 2003-663499/62.

XX New chimeric polypeptides and nucleic acids, useful for detecting and
 PT measuring protease activity, for identifying modulators of protease
 PT activity for detecting and for preventing or ameliorating Alzheimer's
 PT disease.

XX Claim 14; SEQ ID NO 3; 41pp; English.

XX The invention relates to a novel chimeric nucleic acid encoding a
 CC polypeptide which comprises first, second and third domains, where the
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic
 CC reticulum (ER) retention signal peptide, the second domain comprises a
 CC protease cleavage site and the third domain comprises a reporter molecule
 CC and where the protease cleavage site is between the Golgi retention
 CC signal peptide and the reporter molecule. The molecules of the invention
 CC demonstrate nontropic and neuroprotective activities and may be useful
 CC for detecting and measuring protease activity or for identifying
 CC modulators of protease activity in order to detect, prevent or ameliorate
 CC Alzheimer's disease. The current sequence is that of the beta-secretase
 CC cleavage site peptide SEQ ID 3 of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 7; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 3 VKMDAEF 9

RESULT 142
ADC10532
ID ADC10532 standard; peptide; 9 AA.
XX
AC ADC10532;
XX
DT 18-DEC-2003 (first entry)
XX
DE Synthetic beta secretase substrate, SEQ ID NO:8.
XX
KW Substituted hydroxyethylamine; beta secretase inhibitor;
KW amyloid precursor protein; APP; amyloid beta peptide; A beta;
KW neurodegenerative disorder; Alzheimer's disease;
KW mild cognitive impairment; MCI; Down's syndrome;
KW Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-type;
KW HCHWAD; cerebral amyloid angiopathy; degenerative dementia;
KW Parkinson's disease; progressive supranuclear palsy;
KW cortical basal degeneration;
KW diffuse Lewy body type of Alzheimer's disease; lobar haemorrhage;
KW neurotropic; neuroprotective; cerebroprotective; haemostatic; vasotropic;
KW synthetic substrate.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Cleavage-site 5..6
FT /note= "Beta secretase cleavage site"
XX
XX WO2003072535-A2.
XX
XX 04-SEP-2003.
XX
XX 27-FEB-2003; 2003WO-US007287.
XX
XX 27-FEB-2002; 2002US-0359953P.
XX
XX (ELAN-) ELAN PHARM INC.
XX (PHAA) PHARMACIA & UPJOHN.
XX
XX Varghese J, Jagodzinska B, Maillard M, Beck JP, Tenbrink RE;
XX Getman D;
XX
XX WPI; 2003-731584/69.
XX
XX New substituted hydroxyethylamines, useful for the treatment of
XX Alzheimer's disease, mild cognitive impairment and dementia, are beta-
XX secretase, beta-amyloid peptide production inhibitor, and beta-deposition
XX inhibitors.
XX
XX Example D; Page 428; 483pp; English.

The invention relates to substituted hydroxyethylamines or their salts
which are of use in the treatment of Alzheimer's disease and other
neurodegenerative disorders. The compounds act as beta secretase
inhibitors, preventing the cleavage of amyloid precursor protein (APP) to
form the amyloid beta (A beta) peptide. The amyloid beta peptide is
deposited as plaques, which is thought to play a key role in the
pathogenesis of Alzheimer's disease. The compounds of the invention may
be used for the treatment or prevention of Alzheimer's disease, mild
cognitive impairment (MCI), Down's syndrome, Hereditary Cerebral
Haemorrhage with Amyloidosis of the Dutch-type (HCHWAD), cerebral amyloid
angiopathy, other degenerative dementias (including dementias of mixed
vascular and degenerative origin, dementia associated with Parkinson's
disease, dementia associated with progressive supranuclear palsy,
dementia associated with cortical basal degeneration) and diffuse Lewy
body type of Alzheimer's disease. The compounds are also useful in

CC preventing or delaying the onset of Alzheimer's disease in those who
CC would progress from mild cognitive impairment to Alzheimer's disease, and
CC for preventing the potential consequences of cerebral amyloid angiopathy
CC (i.e., single and recurrent lobar haemorrhages). Sequences ADC10529-
CC ADC10531 represent synthetic substrates which can be used to assay beta-
CC secretase activity in the presence or absence of test compounds of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 7; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 143
ADD80769
ID ADD80769 standard; peptide; 9 AA.
XX
AC ADD80769;
XX
DT 29-JAN-2004 (first entry)
XX
DE Synthetic APP-like peptide #6.
XX
KW APP; amyloid precursor protein; Alzheimer's disease; beta-secretase;
KW neurotropic; neuroprotective; cerebroprotective; haemostatic;
KW mild cognitive impairment; MCI; Down's syndrome;
KW hereditary cerebral haemorrhage; Dutch-type amyloidosis;
KW cerebral amyloid angiopathy; degenerative dementia; diffuse Lewy body;
KW amyloid beta protein.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Cleavage-site 5..6
FT /note= "Beta secretase cleavage site"
XX
XX US2003109559-A1.
XX
XX 12-JUN-2003.
XX
XX 11-JUL-2002; 2002US-00193044.
XX
XX 11-JUL-2001; 2001US-0304525P.
XX 30-JUL-2001; 2001US-0308756P.
XX 17-DEC-2001; 2001US-0341341P.
XX 17-DEC-2001; 2001US-0341416P.
XX 21-DEC-2001; 2001US-0344872P.
XX 14-MAY-2002; 2002US-0380574P.
XX
XX (GAIL/) GAILUNAS A.
XX (TUCK/) TUCKER J A.
XX (TENB/) TENBRINK R.
XX (MICK/) MICKELSON J.
XX
XX Gailunas A, Tucker JA, Tenbrink R, Mickelson J;
XX WPI; 2003-863424/80.
XX
XX New N-(3-amino-2-hydroxy-propyl)substituted alkylamide compounds are beta
XX -secretase activity inhibitors, useful for treating e.g. Alzheimer's
XX disease, Down's syndrome, mild cognitive impairment, cerebral amyloid
XX angiopathy.
XX
XX Example D; SEQ ID NO 8; 70pp; English.
XX
XX The invention relates to N-(3-Amino-2-hydroxy-propyl) substituted
XX alkylamide compounds (of structure detailed in the specification) or

CC their salts. Also included is the preparation of the N-(3-Amino-2-hydroxy
CC -propyl) substituted alkylamide compounds. The compounds are useful in a
CC medicament for treating, preventing or delaying the onset of Alzheimer's
CC disease, for treating mild cognitive impairment (MCI), Down's syndrome, a
CC human having a hereditary cerebral haemorrhage with amyloidosis of the
CC Dutch-type, cerebral amyloid angiopathy, other degenerative dementias and
CC diffuse Lewy body type of Alzheimer's disease. The compounds are potent
CC amyloid beta peptide production inhibitors, hence slow down the
CC progression of Alzheimer's disease and prevent the disease in the initial
CC phases. The present sequence is a synthetic peptide containing a beta
CC secretase cleavage site similar to that of APP (amyloid precursor
CC protein), used to test the compounds of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
DB 3 VNLDAEF 9

RESULT 144

AD36577
ID ADE36577 standard; peptide; 9 AA.

AC ADE36577;

DT 29-JAN-2004 (first entry)

DE APP epitope spanning the beta-secretase cleavage site SEQ ID NO:5.

XX immune response; beta-secretase cleavage site; amyloid precursor protein;
KW APP; nontropic; neuroprotective; vaccine; passive immunisation;
KW Alzheimer's disease.

XX Synthetic.

OS Homo sapiens.

XX WO2003076455-A2.

XX 18-SEP-2003.

XX 04-MAR-2003; 2003WO-US006388.

XX 05-MAR-2002; 2002US-0361344P.

XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (MCIN/) MCINNIS P.

XX Solomon B;

XX WPI; 2003-865017/80.

XX Immunizing composition, useful for treating Alzheimer's disease by
PT inhibiting processing of amyloid precursor protein, also antibodies for
PT passive immunization.

XX Claim 5; SEQ ID NO 5; 76pp; English.

XX The present invention describes an immunising composition (A) comprising:
CC (a) an antigenic product (I) which induces an immune response against the
CC beta-secretase cleavage site of amyloid precursor protein (APP); and (b)
CC a carrier, diluent, excipient, adjuvant or auxiliary. Also described: (1)
CC a molecule (II) comprising the antigen-binding part of an antibody (Ab)
CC directed against the beta-secretase cleavage site of APP; (2) a
CC filamentous bacteriophage (FB) that displays (II), where this is a single
CC -chain Ab, on its surface; and (3) a composition containing FB. (A) has
CC nontropic and neuroprotective activities, and can be used in vaccines or
CC passive immunisation. (A) inhibits the cleavage of APP and so prevents
CC the formation of beta-amyloid. (A) can be used to induce an immune

CC response against the beta-secretase cleavage site of APP, specifically
CC for treatment and prevention of Alzheimer's disease. The molecule (II)
CC that contains the antigen-binding part of an Ab directed against the
CC cleavage site, or a filamentous phage that displays such an Ab (as a
CC single-chain molecule) can be used similarly, for passive immunisation.
CC The present sequence represents an APP epitope spanning the beta-
CC secretase cleavage site, which is used in the exemplification of the
CC present invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
DB 1 VKMDAEF 7

RESULT 145

ADG91228

ID ADG91228 standard; peptide; 9 AA.

XX AC ADG91228;

XX 11-MAR-2004 (first entry)

XX Synthetic oligopeptide substrate SEQ ID NO:8.

XX Alzheimer's disease; mild cognitive impairment; Down's syndrome;
KW hereditary cerebral haemorrhage; amyloidosis; aryl alkanolic acid amide;
KW nontropic; neuroprotective; cerebroprotective; haemostatic;
KW beta-secretase activity inhibitor;
KW beta-amyloid peptide production inhibitor; A-beta production inhibitor;
KW A-beta deposition inhibitor;
KW amyloid precursor protein cleavage inhibitor; APP cleavage inhibitor;
KW cerebral amyloid angiopathy; haemorrhage; degenerative dementia;
KW Parkinson's disease; APP substrate.

XX Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note= "biotinylated"

XX WO2003103653-A1.
XX 18-DEC-2003.

XX 11-JUN-2003; 2003WO-US018517.

XX 11-JUN-2002; 2002US-0387880P.

XX (ELAN-) ELAN PHARM INC.

XX John V, Maillard M;

XX WPI; 2004-108264/11.

XX Use of aryl alkanolic acid amides as Beta-secretase activity inhibitors
PT for treating e.g. Alzheimer's disease and Down's syndrome.

XX Example D; SEQ ID NO 8; 363pp; English.

XX The present invention describes a method for the treatment or prevention
CC of e.g. Alzheimer's disease, mild cognitive impairment, Down's syndrome,
CC hereditary cerebral haemorrhage with amyloidosis of the Dutch-type
CC involves use of aryl alkanolic acid amides (I) or their salts. Also
CC described is a method for the preparation of (I). (I) has nontropic,
CC neuroprotective, cerebroprotective and haemostatic activities, and can be
CC used as an inhibitor of beta-secretase activity, beta-amyloid peptide (A-
CC beta) production, A-beta deposition, and amyloid precursor protein (APP)

CC cleavage. (I) can be used for treating, preventing or delaying the onset
 CC of the Alzheimer's disease, for treating mild cognitive impairment,
 CC Down's syndrome, hereditary cerebral haemorrhage with amyloidosis of the
 CC Dutch-type, cerebral amyloid angiopathy and preventing its potential
 CC consequences i.e. single and recurrent lobar haemorrhages, other
 CC degenerative dementia (including dementia of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration) or diffuse Lewy body type of
 CC Alzheimer's disease. The compounds (I) inhibit beta-secretase, an enzyme
 CC that cleaves APP to produce A-beta peptide, a major component of the
 CC amyloid plaques found in the brains of Alzheimer's sufferers. The present
 CC sequence represents a synthetic oligopeptide substrate, which is used in
 CC an example from the present invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 146

ADJ71557
 ID ADJ71557 standard; peptide; 9 AA.

XX AC

XX ADJ71557;

XX 06-MAY-2004 (first entry)

XX N-terminal APP peptide C-terminal fragment, SEQ ID 220.

XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 XX amyloid precursor protein; APP; Alzheimer's disease.

XX Homo sapiens.

XX WO2004013172-A2.

XX 12-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007833.

XX 24-JUL-2002; 2002EP-00447147.

XX 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;

XX WPI; 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 XX Alzheimer's disease.

XX Claim 7; Page 67; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 |:::|
 Db 2 VKMDAEF 8

RESULT 147

ADJ71567
 ID ADJ71567 standard; peptide; 9 AA.

XX AC

XX ADJ71567;

XX 06-MAY-2004 (first entry)

XX N-terminal APP peptide C-terminal fragment, SEQ ID 230.

XX Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 XX amyloid precursor protein; APP; Alzheimer's disease.

XX Homo sapiens.

XX WO2004013172-A2.

XX 12-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007833.

XX 24-JUL-2002; 2002EP-00447147.

XX 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;

XX WPI; 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

XX Claim 7; Page 67; 104pp; English.

XX The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
 |:::|
 Db 1 VKMDAEF 7

RESULT 148

ADJ71546
 ID ADJ71546 standard; peptide; 9 AA.

XX AC

XX ADJ71546;

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DT 06-MAY-2004 (first entry)
XX
DE N-terminal APP peptide C-terminal fragment, SEQ ID 209.
XX
KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
KW amyloid precursor protein; APP; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2004013172-A2.
XX
PD 12-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007833.
XX
PR 24-JUL-2002; 2002EP-00447147.
PR 06-AUG-2002; 2002US-0401497P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Delacourte A, Sergeant N;
XX
DR WPI; 2004-180423/17.
XX
PT New beta-amyloid or amyloid precursor protein preparation, useful as a
PT prophylactic vaccine or a therapeutic for preventing or treating a
PT disease associated with beta-amyloid formation and/or aggregation, e.g.
PT Alzheimer's disease.
XX
PS Claim 7; Page 67; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
3 VKWDAEF 9

RESULT 149
ADJ47996
ID ADJ47996 standard; peptide; 9 AA.
XX
AC ADJ47996;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human BACE peptide substrate cleavage site SEQ ID NO:1.
XX
KW N-substituted-2-oxo-3-substituted amino-pyrrolidine; nootropic;
KW neuroprotective; cerebroprotective; gamma-lactam; beta-secretase; BACE;
KW Alzheimer's disease; cerebral amyloid angiopathy; Down's Syndrome.
XX
OS Unidentified.
XX
PN WO2004013098-A1.
XX
PD 12-FEB-2004.
XX
PF 05-AUG-2003; 2003WO-US024407.
XX

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PR 05-AUG-2002; 2002US-0401390P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Decicco CP, Tebben AJ, Thompson LA, Combs AP;
XX
DR WPI; 2004-226340/21.
XX
PT New N-substituted-2-oxo-3-substituted amino-pyrrolidine derivatives are
PT beta-secretase inhibitors used for treating e.g. Alzheimer's disease,
PT cerebral amyloid angiopathy and Down's Syndrome.
XX
PS Disclosure; SEQ ID NO 1; 156pp; English.
XX
CC The invention relates to novel N-substituted-2-oxo-3-substituted amino-
CC pyrrolidine derivatives (I). A compound of the invention has nootropic,
CC neuroprotective, and cerebroprotective activity. The compounds of the
CC invention are useful for the treatment of Alzheimer's disease, cerebral
CC amyloid angiopathy and Down's Syndrome. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
2 VNLDAEF 8

RESULT 150
ADM16649
ID ADM16649 standard; peptide; 9 AA.
XX
AC ADM16649;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligopeptide substrate of the invention #1.
XX
KW 1; 3-Diamino-2-hydroxypropane; Alzheimer's disease;
KW mild cognitive impairment; Down's syndrome;
KW hereditary cerebral hemorrhage; Parkinson's disease; APP substrate.
XX
OS Synthetic.
XX
PN WO2004022523-A2.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-US028116.
XX
PR 06-SEP-2002; 2002US-0408783P.
XX
PA (ELAN-) ELAN PHARM INC.
PA (PHAA ) PHARMACIA & UPJOHN.
XX
PI Fobian YM, Freskos JN, Jagodzinska B;
XX
DR WPI; 2004-315550/29.
XX
PT New 1,3-diamino-2-hydroxypropane derivatives are beta-secretase and
PT amyloid beta peptide production inhibitors used for treating e.g.
PT Alzheimer's disease and cerebral amyloid angiopathy.
XX
PS Example; SEQ ID NO 8; 535pp; English.
XX
CC The present invention relates to 1,3-Diamino-2-hydroxypropane derivatives
CC and their salts. Used for treatment or prevention of Alzheimer's disease,
CC mild cognitive impairment, Down's syndrome, hereditary cerebral
CC hemorrhage with amyloidosis of the Dutch-type, cerebral amyloid
CC

```

CC angiopathy, other degenerative dementias, dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia,
 CC associated with cortical basal degeneration or diffuse Lewy body type of
 CC Alzheimer's disease. The present sequence represents a synthetic
 CC oligopeptide substrate of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 151
 ADM32517
 ID ADM32517 standard; peptide; 9 AA.

XX AC ADM32517;

XX DT 17-JUN-2004 (first entry)

XX DE Synthetic beta secretase substrate, SEQ ID NO:8.

XX KW Acetyl 2-hydroxy-1,3-diaminoalkane; beta secretase inhibitor;
 KW amyloid precursor protein; APP; amyloid beta peptide; A beta;
 KW neurodegenerative disorder; Alzheimer's disease;
 KW mild cognitive impairment; MCI; Down's syndrome;
 KW Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch-type;
 KW HCHWAD; cerebral amyloid angiopathy; degenerative dementia;
 KW Parkinson's disease; progressive supranuclear palsy;
 KW cortical basal degeneration;
 KW diffuse Lewy body type of Alzheimer's disease; lobar haemorrhage;
 KW neurotropic; neuroprotective; cerebroprotective; haemostatic;
 KW antiparkinsonian; vasotropic; synthetic substrate.
 XX
 OS Synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 5..6 /note= "Beta secretase cleavage site"

XX PN WO2004024081-A2.

XX PD 25-MAR-2004.

XX PF 10-SEP-2003; 2003WO-US028503.

XX PR 10-SEP-2002; 2002US-0409453P.

XX PR 05-MAR-2003; 2003US-0452231P.

XX PR 01-AUG-2003; 2003US-0491757P.

XX PA (ELAN-) ELAN PHARM INC.

XX PA (PFIZ-) PFIZER INC.

XX PI Maillard M, Baldwin ET, Beck JT, Hughes R, John V, Pulley SR;

XX PI Tenbrink R;

XX DR WPI; 2004-329385/30.

XX PS Example D; SEQ ID NO 8; 459pp; English.

XX CC The invention relates to acetyl 2-hydroxy-1,3-diaminoalkanes or their
 CC salts which are of use in the treatment of Alzheimer's disease and other
 CC neurodegenerative disorders. The compounds act as beta secretase

CC inhibitors, preventing the cleavage of amyloid precursor protein (APP) to
 CC form the amyloid beta (A beta) peptide. The amyloid beta peptide is
 CC deposited as plaques, which is thought to play a key role in the
 CC pathogenesis of Alzheimer's disease. The compounds of the invention may
 CC be used for the treatment or prevention of Alzheimer's disease, mild
 CC cognitive impairment (MCI), Down's syndrome, Hereditary Cerebral
 CC Haemorrhage with Amyloidosis of the Dutch-type (HCHWAD), cerebral amyloid
 CC angiopathy, other degenerative dementias (including dementias of mixed
 CC vascular and degenerative origin, dementia associated with Parkinson's
 CC disease, dementia associated with progressive supranuclear palsy,
 CC dementia associated with cortical basal degeneration) and diffuse Lewy
 CC body type of Alzheimer's disease. The compounds are also useful in
 CC preventing or delaying the onset of Alzheimer's disease in those who
 CC would progress from mild cognitive impairment to Alzheimer's disease, and
 CC for preventing the potential consequences of cerebral amyloid angiopathy
 CC (i.e., single and recurrent lobar haemorrhages). Sequences ADM32515-
 CC ADM32518 represent synthetic substrates which can be used to assay beta-
 CC secretase activity in the presence or absence of test compounds of the
 CC invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 152

ID ADM32591

XX ID ADO43591 standard; peptide; 9 AA.

XX AC ADO43591;

XX DT 29-JUL-2004 (first entry)

XX DE Synthetic peptide #1 cleavable by beta-secretase.

XX KW amyloid precursor protein; APP; beta-secretase; beta-amyloid plaque;
 KW beta-amyloid; Alzheimer's disease; mild cognitive impairment;
 KW Down's syndrome; Hereditary Cerebral Haemorrhage;
 KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;
 KW Parkinson's disease; frontotemporal dementia; parkinsonism;
 KW progressive supranuclear palsy; cortical basal degeneration.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "biotin attached"

FT Cleavage-site 5..6

XX PN WO2004037179-A2.

XX PD 06-MAY-2004.

XX XX 21-OCT-2003; 2003WO-US033312.

XX PR 21-OCT-2002; 2002US-0420062P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Beck JT;

XX DR WPI; 2004-375813/35.

XX PT Use of substituted peptides for inhibition of cleavage of an amyloid
 PT precursor protein isotype at a site in the isotype susceptible to
 PT cleavage.
 XX

PS Example E; Page 62; 126pp; English.

XX The specification describes a method for the inhibition of cleavage of an

CC amyloid precursor protein (APP) isotype at a site in the APP isotype

CC susceptible to cleavage. The method involves contacting the APP isotype

CC with a substituted peptide of a formula given in the specification. The

CC substituted peptides of the invention are useful for inhibition of beta-

CC secretase activity, for inhibition of cleavage of an APP, for inhibition

CC of production of amyloid beta peptide and beta-amyloid plaques in animal

CC cell, and for the manufacture of a medicament for the treatment or

CC prevention of disease characterized by beta-amyloid deposits in brain

CC (such as Alzheimer's disease). They are also useful for helping prevent

CC or delay the onset of Alzheimer's disease, mild cognitive impairment,

CC Down's syndrome, Hereditary Cerebral Haemorrhage with amyloidosis of the

CC Dutch-Type, cerebral amyloid angiopathy and preventing its potential

CC consequences i.e. single and recurrent lobar haemorrhages, degenerative

CC dementia's (e.g. dementia's of mixed vascular and degenerative origin,

CC dementia associated with Parkinson's disease, frontotemporal dementia

CC with parkinsonism, and dementia associated with progressive supranuclear

CC palsy and cortical basal degeneration) and diffuse Lewy body type of

CC Alzheimer's disease. ADO43591-ADO43592 represent synthetic substrates for

CC cleavage by beta-secretase. They were used to assay beta-secretase

CC activity in the presence and absence of substituted peptides of the

CC invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;

Best Local Similarity 57.1%; Pred. NO. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

DB 3 VNLDAPF 9

RESULT 153

ADN88513

ID ADN88513 standard; peptide; 9 AA.

AC ADN88513;

XX

DT 12-AUG-2004 (first entry)

XX

DE Fluorogenic protease indicator peptide #209.

XX

KW fluorogenic; protease detection; protease inhibitor.

XX

OS Synthetic.

XX

PN US2004096926-A1.

XX

PD 20-MAY-2004.

XX

PF 04-JUN-2001; 2001US-00874350.

XX

PR 20-FEB-1997; 97US-00802981.

XX

PR 20-FEB-1998; 98WO-US0003000.

XX

PR 10-SEP-1999; 99US-00394019.

XX

PR 11-SEP-2000; 2000WO-US024882.

XX

PA (ONCO-) ONCOIMMUNIN INC.

XX

PI Packard BS, Komoriya A;

XX

DR WPI; 2004-399235/37.

XX

PT Fluorogenic composition useful for detecting protease activity and test

PT substance modulating protease activity.

XX

PS Claim 1; SEQ ID NO 209; 114pp; English.

XX

CC The invention relates to a fluorogenic composition (I) for detecting the

CC activity of a protease. (I) is useful for detecting the activity of a

CC protease, which involves contacting the protease with (I), where the

CC activity of protease is detected in a histological section, cell culture

CC or tissue section. The cell suspension is derived from the biological

CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The

CC protease activity is detected by fluorescence microscopy, fluorescence

CC microplate reader, absorption microplate reader, flow cytometry,

CC fluorometry, absorption spectroscopy or confocal, fluorescent microplate

CC reader. (I) is useful for delivering a molecule into a cell, and for

CC screening a test agent for the ability to modulate the activity of the

CC protease. (I) is useful for detection and localisation of protease

CC activity in biological samples. (I) also acts as a protease inhibitor,

CC thus useful as protease inhibitors. (I) enables detection of the protease

CC activity, and provides a high intensity fluorescent signal at a visible

CC wavelength when they are digested by a protease. The present sequence

XX represents a fluorogenic protease indicator peptide of the invention.

SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;

Best Local Similarity 57.1%; Pred. NO. 1.8e+06;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

DB 3 VNLDAPF 9

RESULT 154

ADP43057

ID ADP43057 standard; peptide; 9 AA.

XX

AC ADP43057;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic APP substrate, SEQ ID NO 8.

XX

KW substituted aminoether; inhibitor; beta-secretase; cleavage;

KW amyloid precursor protein; APP; amyloid beta; Alzheimer's disease;

KW neuroprotective; nootropic; cerebroprotective; haemostatic;

KW antiparkinsonian; mild cognitive impairment; Down's syndrome;

KW hereditary Cerebral haemorrhage; amyloidosis; Dutch-Type;

KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;

KW Parkinson's disease; progressive supranuclear palsy;

KW cortical basal degeneration; diffuse Lewy body type; APP substrate.

XX

OS Synthetic.

XX

PN WO2004024675-A1.

XX

PD 25-MAR-2004.

XX

PF 10-SEP-2003; 2003WO-US028388.

XX

PR 10-SEP-2002; 2002US-0409565P.

XX

PA (PHAA) PHARMACIA & UPJOHN.

XX

PI Beck JP, Downes M, Warpehoski MA;

XX

DR WPI; 2004-440449/41.

XX

PT New substituted aminoethers are beta-secretase inhibitors useful in the

PT manufacture of medicaments for treating Alzheimer's disease.

XX

PS Example D; SEQ ID NO 8; 122pp; English.

XX

CC The invention relates to novel substituted aminoethers, their salts and

CC esters. The aminoethers are effective inhibitors of beta-secretase, that

CC inhibits beta-secretase mediated cleavage of amyloid precursor protein

CC (APP), that are effective inhibitors of A beta production and/or are

CC effective to reduce amyloid beta deposits or plaques making them

CC efficient therapeutics for slowing the progression of/preventing
 CC Alzheimer's disease. The aminoethers have the following activities:
 CC neuroprotective, nootropic, cerebroprotective, haemostatic, and
 CC antiparkinsonian. The novel substituted aminoethers are useful in the
 CC manufacture of a medicament. The medicament is useful in the treatment,
 CC prevention or delaying the onset of Alzheimer's disease, for treating
 CC patients with mild cognitive impairment, treating Down's syndrome,
 CC hereditary cerebral haemorrhage with amyloidosis of the Dutch-Type,
 CC cerebral amyloid angiopathy and preventing its potential consequences,
 CC e.g. single and recurrent lobar haemorrhages, for treating other
 CC degenerative dementias, including dementias of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy, dementia
 CC associated with cortical basal degeneration, and diffuse Lewy body type
 CC of Alzheimer's disease. This sequence represents a synthetic APP
 CC substrate that can be cleaved by beta-secretase, used to assay beta-
 CC secretase activity in the presence or absence of the inhibitory compounds
 CC of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 |:::|
 DB 3 VNLDAEF 9

RESULT 155
 ADP45545
 ID ADP45545 standard; peptide; 9 AA.

XX AC ADP45545;

XX DT 09-SEP-2004 (first entry)

XX DE Novel urea and carbamate derivative-related substrate peptide SeqID8.

XX KW substituted urea; carbamate derivative; nootropic; neuroprotective;
 KW haemostatic; cerebroprotective; antiparkinsonian;
 KW beta-secretase enzyme inhibitor;
 KW beta-secretase-mediated-APP cleavage inhibitor;
 KW amyloid beta peptide production inhibitor; Alzheimer's disease;
 KW mild cognitive impairment; MCI; Down's syndrome;
 KW Hereditary Cerebral Haemorrhage; Amyloidosis; Dutch-Type;
 KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;
 KW Parkinson's disease; progressive supranuclear palsy;
 KW cortical basal degeneration; diffuse Lewy body; substrate.
 XX

OS Unidentified.
 OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Cleavage-site 5..6

XX PN WO2004050609-A1.

XX PD 17-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US037998.

XX PR 27-NOV-2002; 2002US-0429769P.

XX PA (ELAN-) ELAN PHARM INC.
 XX PA (PHAA) PHARMACIA & UPJOHN CO.
 XX PA (PULL/) PULLEY S R.
 XX PA (TUKER/) TUKER J A.

XX DR WPI; 2004-480588/45.

XX PT New substituted urea and carbamate derivatives are beta-secretase enzyme

PT inhibitors useful to treat e.g. Alzheimer's disease and Down's syndrome.
 XX
 PS Example D; SEQ ID NO 8; 213pp; English.
 XX
 CC This invention relates to novel substituted urea and carbamate
 CC derivatives and their salts or solvates. The invention may be useful for
 CC the production of compounds with a nootropic, neuroprotective,
 CC haemostatic, cerebroprotective or antiparkinsonian activity acting as
 CC beta-secretase enzyme inhibitors, beta-secretase-mediated-APP cleavage
 CC inhibitors or amyloid beta (A beta) peptide production inhibitors. The
 CC invention may be useful to treat or prevent Alzheimer's disease (AD), to
 CC prevent or delay the onset of AD, to treat mild cognitive impairment
 CC (MCI), to treat or prevent or delaying the onset of AD in patients (Chose
 CC who would progress from MCI to AD), to treat Down's syndrome, to treat
 CC humans with Hereditary Cerebral Haemorrhage with Amyloidosis of the Dutch
 CC -Type, to treat cerebral amyloid angiopathy and preventing its potential
 CC consequences (single or recurrent lobar haemorrhages) and to treat other
 CC degenerative dementia's, including dementia's of mixed vascular and
 CC degenerative origin, dementia associated with Parkinson's disease,
 CC dementia associated with progressive supranuclear palsy and dementia
 CC associated with cortical basal degeneration and diffuse Lewy body type of
 CC AD. The present sequence is that of a substrate peptide which was used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
 |:::|
 DB 3 VNLDAEF 9

RESULT 156

ADQ91626

ID ADQ91626 standard; peptide; 9 AA.

XX AC ADQ91626;

XX DT 21-OCT-2004 (first entry)

XX DE Peptide substrate for beta-amyloid converting enzyme.

XX KW Beta-amyloid converting enzyme; BACE; inhibitor; triazine;
 KW Alzheimer's disease; neuroprotective; nootropic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT Modified-site 9 /note= "N-terminal EDANS donor"

XX FT Modified-site 9 /note= "C-terminal DABCYL quenching acceptor"

XX PN WO2004063196-A1.

XX PD 29-JUL-2004.

XX PF 12-JAN-2004; 2004WO-GB0000062.

XX PR 14-JAN-2003; 2003GB-00000804.

XX PA (NOVO-) DE NOVO PHARM LTD.

XX PI Willems H, Harris W, John DE;

XX DR WPI; 2004-561868/54.

XX PT New and known optionally heterofused 1,2,4-triazin-3-yl-hydrazine
 PT derivatives, useful for manufacture of a medicament for treating
 PT Alzheimer's disease, are beta-amyloid converting enzyme inhibitors.

XX Example 37; Page 25; 36pp; English.

PS The present sequence is that of a fluorescently labelled peptide

CC substrate for beta-amyloid converting enzyme (BACE). The peptide becomes

CC slightly fluorescent upon enzymatic cleavage due to disruption of the

CC resonance energy transfer between the N-terminal EDANS donor and C-

CC terminal DABCYL quenching acceptor in the intact substrate. It was used

CC in an example from the invention in an assay of the BACE inhibitor

CC activity of triazine compounds of the invention. Such compounds may have

CC utility in the treatment or prevention of diseases or conditions in which

CC BACE is implicated, especially a disease or condition associated with the

CC deposition and/or elevated levels of amyloid beta peptide, e.g.

CC Alzheimer's disease.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 7; DB 8; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7

Db 2 VNLDAEF 8

RESULT 157

AAR22054

ID AAR22054 standard; peptide; 10 AA.

AC AAR22054;

XX

DT 25-MAR-2003 (revised)

DT 06-JUL-1992 (first entry)

XX

DE Peptide P1.

XX

KW Beta amyloid; protein precursor; protease; Alzheimers disease;

KW radioiodination.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "site of radioiodination"

FT

XX WO9203542-A.

XX

PD 05-MAR-1992.

XX

PF 19-AUG-1991; 91WO-U0005932.

XX

PR 17-AUG-1990; 90US-00568806.

XX

PA (UYBO-) UNIV BOSTON.

XX

PI Abraham CR;

XX

DR WPI; 1992-096886/12.

XX

PT Treatment and diagnosis of Alzheimer's disease - by reducing beta-protein

PT precursor proteolysis near beta-protein N-terminus by administering

PT proteolysis inhibitor.

XX

PS Disclosure; Page 6; 29pp; English.

XX

CC The synthetic peptide substrate P1 was used to assay for proteases that

CC cleave in the vicinity of the N-terminus of the amyloid beta protein. The

CC peptide corresponds to the beta protein precursor sequence flanking that

CC site. The peptide starts five amino acids upstream from the N-terminus

CC (at Asp) of the beta protein, and extends across the putative cleavage

CC site into the beta protein itself. Histidine was substituted for the

CC native isoleucine to give a site for radioiodination. Labelled peptide

CC was incubated with brain fractions from Alzheimers disease patients. The

CC resulting fragments were separated by TLC and N-terminal fragments

CC detected by autoradiography. See also AAR22055.6. (Updated on 25-MAR-2003

XX to correct PA field.)

SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.2e+02; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7

Db 4 VKMDAEF 10

RESULT 158

AAR24263

ID AAR24263 standard; protein; 10 AA.

XX

AC AAR24263;

XX

DT 25-MAR-2003 (revised)

DT 09-NOV-1992 (first entry)

XX

DE Human amyloidin protease substrate sequence #3.

XX

KW Alzheimer's disease; beta amyloid precursor protein; APP; zinc;

KW metalloprotease; hAP; protease inhibitor; APP592-601.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "Acetylated-Ser"

FT

XX WO9207068-Al.

XX

PD 30-APR-1992.

XX

PF 04-OCT-1991; 91WO-US007290.

XX

PR 05-OCT-1990; 90US-00594122.

PR 30-SEP-1991; 91US-00766351.

XX

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PA (ELIL) LILLY & CO ELI.

XX

PI Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;

PI Johnstone EM;

XX

DR WPI; 1992-167148/20.

XX

PT Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like

PT substrate for identifying protease inhibitors.

XX

PS Example 5; Page 29; 62pp; English.

XX

CC This synthetic substrate is based on the sequence of residues 592 to 601

CC of the 695 amino acid App. Met596 has been replaced by Ala. Amyloidin

CC cleaves the Lys-Ala and Asp-Ala bonds of this peptide. See AAR24260-3,

CC AAR24266-7 and AAQ24875-Q24887. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.2e+02; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7

Db 3 VKADAEF 9


```

RESULT 159
AAR24267
ID AAR24267 standard; protein; 10 AA.
XX
AC AAR24267;
XX
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
XX Human amyloidin protease substrate sequence #5.
DE
XX Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor; APP592-601.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetylated-Ser"
FT
FT Cleavage-site 4. .5
FT Cleavage-site 5. .6
FT Modified-site 5
FT /label= Nle
FT Cleavage-site 6. .7
FT Cleavage-site 7. .8
XX
XX WO9207068-A1.
XX
XX 30-APR-1992.
XX
XX 04-OCT-1991; 91WO-US007290.
XX
XX 05-OCT-1990; 90US-00594122.
PR 30-SEP-1991; 91US-00766351.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
PA (ELIL ) LILLY & CO ELI.
XX
XX Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
PI Johnstone EM;
XX
XX WPI; 1992-167148/20.
XX
XX Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
PT substrate for identifying protease inhibitors.
XX
XX Example 5; Page 29; 62pp; English.
XX
XX This synthetic substrate is based on the sequence of residues 592 to 601
CC of the 695 amino acid APP. Met596 has been replaced by Nle. Amyloidin
CC cleaves the peptide in 4 places. The substrate can be used in an assay
CC for identifying inhibitors of proteases which cleave Met-Asp bonds, e.g.
CC amyloidin, human skin chymase or rat mast cell protease I or II. See
CC AAR24260-3, AAR24266 and AAQ24875-Q24887. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VKXDAEF 9
|:|:|

RESULT 160
AAR24262
ID AAR24262 standard; protein; 10 AA.
XX
XX
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
XX Human amyloidin protease substrate sequence #4.
DE
XX Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor; APP592-601.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetylated-Ser"
FT
FT Cleavage-site 4. .5
FT Cleavage-site 5. .6
FT Modified-site 5
FT /label= Nle
FT Cleavage-site 6. .7
FT Cleavage-site 7. .8
XX
XX WO9207068-A1.
XX
XX 30-APR-1992.
XX
XX 04-OCT-1991; 91WO-US007290.
XX
XX 05-OCT-1990; 90US-00594122.
PR 30-SEP-1991; 91US-00766351.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
PA (ELIL ) LILLY & CO ELI.
XX
XX Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
PI Johnstone EM;
XX
XX WPI; 1992-167148/20.
XX
XX Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
PT substrate for identifying protease inhibitors.
XX
XX Example 5; Page 29; 62pp; English.
XX
XX This synthetic substrate is based on the sequence of residues 592 to 601
CC of the 695 amino acid APP. Met596 has been replaced by Nle. Amyloidin
CC cleaves the peptide in 4 places. The substrate can be used in an assay
CC for identifying inhibitors of proteases which cleave Met-Asp bonds, e.g.
CC amyloidin, human skin chymase or rat mast cell protease I or II. See
CC AAR24260-3, AAR24266 and AAQ24875-Q24887. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VKXDAEF 9
|:|:|

```

```

AAR24262;
AC
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
XX Human amyloidin protease substrate sequence #2.
DE
XX Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor; APP592-601.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetylated-Ser"
FT
FT WO9207068-A1.
XX
XX 30-APR-1992.
XX
XX 04-OCT-1991; 91WO-US007290.
XX
XX 05-OCT-1990; 90US-00594122.
PR 30-SEP-1991; 91US-00766351.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
PA (ELIL ) LILLY & CO ELI.
XX
XX Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
PI Johnstone EM;
XX
XX WPI; 1992-167148/20.
XX
XX Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
PT substrate for identifying protease inhibitors.
XX
XX Example 5; Page 29; 62pp; English.
XX
XX This synthetic substrate is based on the sequence of residues 592 to 601
CC of the 695 amino acid APP. Lys595 has been replaced by Gln. Amyloidin
CC cleaves the Met-Asp bond of this peptide but does not cleave any of the
CC other bonds. See AAR24260-3, AAR24266-7 and AAQ24875-Q24887. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VQMDAEF 9
|:|:|

RESULT 161
AAR24266
ID AAR24266 standard; protein; 10 AA.
XX
XX AAR24266;
AC
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
XX Human amyloidin protease substrate sequence #4.
DE
XX Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor; APP592-601.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT

```

```

FT      /note= "Acetylated-Ser"
FT      Cleavage-site 4. .5
FT      Cleavage-site 5. .6
FT      Cleavage-site 6. .7
XX      WO9207068-A1.
XX      30-APR-1992.
XX      04-OCT-1991; 91WO-US007290.
XX      05-OCT-1990; 90US-00594122.
XX      30-SEP-1991; 91US-00766351.
XX      (ATHE-) ATHENA NEUROSCIENCES INC.
XX      (ELIL ) LILLY & CO ELI.
XX      Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
XX      Johnstone EM;
XX      WPI; 1992-167148/20.
XX      Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
XX      substrate for identifying protease inhibitors.
XX      Example 5; Page 29; 62pp; English.
XX      This synthetic substrate is based on the sequence of residues 592 to 601
XX      of the 695 amino acid APP. Lys595 has been replaced by Arg and Arg601 has
XX      been replaced by Lys. Amyloidin cleaves the peptide in 3 places. See
XX      AAR24260-3, AAR24267 and AAQ24875-Q24887. (Updated on 25-MAR-2003 to
XX      correct PN field.)
XX      Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 3 VRMDAEF 9
:::|
:::|

RESULT 162
AAR24260
ID AAR24260 standard; protein; 10 AA.
XX
AC AAR24260;
XX
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
DE Human amyloidin protease generic substrate sequence.
XX
KW Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetylated-Ser"
FT Misc-difference 4
FT /label= Gln, Lys
FT Misc-difference 5
FT /label= Met, Nle
XX
XX WO9207068-A1.
XX
XX 30-APR-1992.
XX
XX 04-OCT-1991; 91WO-US007290.

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XX      05-OCT-1990; 90US-00594122.
XX      30-SEP-1991; 91US-00766351.
XX      (ATHE-) ATHENA NEUROSCIENCES INC.
XX      (ELIL ) LILLY & CO ELI.
XX      Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
XX      Johnstone EM;
XX      WPI; 1992-167148/20.
XX      Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
XX      substrate for identifying protease inhibitors.
XX      Claim 30; Page 52; 62pp; English.
XX      Artificial substrate peptides corresponding to this generic formula are
XX      cleaved by amyloidin (at 1-4 sites, depending on the particular
XX      sequence). They can be used in an assay for identifying inhibitors of
XX      proteases which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase
XX      or rat mast cell protease I or II. See also AAR24261-3, AAR24266-7 and
XX      AAQ24875-Q24887. (Updated on 25-MAR-2003 to correct PN field.)
XX      Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
DB 3 VXXDAEF 9
:::|
:::|

RESULT 163
AAR24261
ID AAR24261 standard; protein; 10 AA.
XX
AC AAR24261;
XX
XX 25-MAR-2003 (revised)
DT 09-NOV-1992 (first entry)
XX
DE Human amyloidin protease substrate sequence #1.
XX
KW Alzheimer's disease; beta amyloid precursor protein; APP; zinc;
KW metalloprotease; hAP; protease inhibitor; APP592-601.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetylated-Ser"
FT
XX WO9207068-A1.
XX
XX 30-APR-1992.
XX
XX 04-OCT-1991; 91WO-US007290.
XX
XX 05-OCT-1990; 90US-00594122.
XX      30-SEP-1991; 91US-00766351.
XX      (ATHE-) ATHENA NEUROSCIENCES INC.
XX      (ELIL ) LILLY & CO ELI.
XX      Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;
XX      Johnstone EM;
XX      WPI; 1992-167148/20.
XX      Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like
XX      substrate for identifying protease inhibitors.

```

PT substrate for identifying protease inhibitors.

PS Claim 1; Page 52; 62pp; English.

XX Claimed human amyloidin protease is defined by its ability to cleave the
CC Met-Asp bond of this synthetic substrate. The substrate, which
CC corresponds to residues 592 to 601 of the 695 amino acid APP, can be used
CC in an assay for identifying inhibitors of proteases which cleave Met-Asp
CC bonds, e.g. amyloidin, human skin chymase or rat mast cell protease I or
CC II. See AAR24260-3, AAR24266-7 and AAQ24875-Q24887. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7

Db 3 VKMDAEF 9

RESULT 164

AAW08362

ID AAW08362 standard; peptide; 10 AA.

AC AAW08362;

DT 05-SEP-1997 (first entry)

DE Beta-secretase substrate #3.

KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1 /note= "acetylated"

PN W09640885-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US0009985.

PR 07-JUN-1995; 95US-00480498.

PR 07-JUN-1995; 95US-00485152.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

PI Chrysler SMS, Sinha S, Keim PS, Anderson JP, Jacobson-Croak KL;

PI Tan H, Mcconlogue LC;

XX WPI; 1997-052304/05.

XX Beta-secretase which specifically cleaves beta-amyloid precursor protein
PT - useful to screen for inhibitors useful in treatment of Alzheimer's
PT disease.

XX Disclosure; Page 45; 92pp; English.

XX AA08359-W08362 represent substrates for the enzyme of the invention. The
CC enzyme of the invention is beta-secretase, and specifically cleaves beta-
CC amyloid precursor protein (beta-APP). Normal processing of beta-APP is
CC thought to occur via cleavage between residues 16 and 17 of the beta-
CC amyloid peptide region by an alpha-secretase. Pathogenic processing is
CC thought to occur by beta-secretase cleavage of beta-APP. Beta-secretase
CC activity can be detected and measured using a method of the invention,
CC which detects at least one of the beta-secretase cleavage products formed
CC on cleavage. The method can be used to determine whether a test substance

CC inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds
CC effective to at least partially inhibit beta-secretase activity can be
CC used to inhibit cleavage of beta-APP in cells or mammalian hosts.
CC Isolation and purification of beta-secretase will permit chemical
CC modelling of a critical event in the pathology of Alzheimer's disease
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7

Db 3 VNLDAEF 9

RESULT 165

AAAY33756

ID AAY33756 standard; protein; 10 AA.

AC AAY33756;

DT 09-NOV-1999 (first entry)

DE Synthetic oligopeptide 5-5'SW.

KW Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW Alzheimer's disease; measure activity; cleavage site.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal Ser is acetylated"

XX US5942400-A.

XX 24-AUG-1999.

PF 07-JUN-1996; 96US-00659984.

PR 07-JUN-1995; 95US-00480498.

PR 07-JUN-1995; 95US-00485152.

XX (ELAN-) ELAN PHARM INC.

XX Sinha S, Jacobson-Croak KL, Anderson JP;

XX WPI; 1999-517417/43.

XX A method for detecting human beta-secretase cleavage of polypeptides
PT useful for identifying beta-secretase inhibitors.

XX Example; Col 30; 43pp; English.

XX Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These synthetic
CC peptides contain the cleavage site of APP. Beta-secretase and APP are
CC used in a method for detecting human beta-secretase cleavage of
CC polypeptides and for identifying beta-secretase inhibitors. Inhibition of
CC beta-secretase activity would be useful for chemical modelling of a
CC critical event in the pathology of Alzheimer's disease. Inhibitors of
CC beta-secretase would be useful for the prevention and treatment of
CC Alzheimer's disease and Down's Syndrome

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;


```

PR 03-MAR-1999; 99US-0122599P.
PA (RHON ) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
DR Polypeptide with beta-secretase activity, specific for wild-type amyloid
XX precursor protein, useful in treating Alzheimer's disease.
PT Example 3; Page 24; 44pp; French.
XX
XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VXXXAEEF 7
Db 3 VNLDAAEF 9
RESULT 169
AAY69710
ID AAY69710 standard; peptide; 10 AA.
XX
XX AAY69710;
XX
XX 11-APR-2000 (first entry)
XX
XX Beta-APP alpha-secretase substrate [KVD]-APP(-5,+5).
XX
XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX cleavage site; beta-secretase; neurodegenerative disease;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO9964587-A1.
XX
XX 16-DEC-1999.
XX
XX 04-JUN-1999; 99WO-FR001326.
XX
XX 05-JUN-1998; 98FR-00007068.
XX
XX 03-MAR-1999; 99US-0122599P.
XX
XX (RHON ) RHONE-POULENC RORER SA.
XX PA
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type amyloid
XX precursor protein, useful in treating Alzheimer's disease.
XX
XX Example 3; Page 24; 44pp; French.
XX

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```

CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VXXXAEEF 7
Db 3 VKVDAEF 9
RESULT 170
AAY69705
ID AAY69705 standard; peptide; 10 AA.
XX
XX AAY69705;
XX
XX 11-APR-2000 (first entry)
XX
XX Beta-APP alpha-secretase substrate [KLD]-APP(-5,+5).
XX
XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX cleavage site; beta-secretase; neurodegenerative disease;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO9964587-A1.
XX
XX 16-DEC-1999.
XX
XX 04-JUN-1999; 99WO-FR001326.
XX
XX 05-JUN-1998; 98FR-00007068.
XX
XX 03-MAR-1999; 99US-0122599P.
XX
XX (RHON ) RHONE-POULENC RORER SA.
XX PA
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type amyloid
XX precursor protein, useful in treating Alzheimer's disease.
XX
XX Example 3; Page 24; 44pp; French.
XX
XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;

```

```

Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  VXXXXAEF 7
      |:::|
Db      3  VKLDAEF 9

RESULT 171
AAy69709
ID  AAY69709 standard; peptide; 10 AA.
AC  AAY69709;
XX
DT  11-APR-2000 (first entry)
XX
DE  Beta-APP alpha-secretase substrate [KID]-APP(-5,+5).
XX
KW  Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW  cleavage site; beta-secretase; neurodegenerative disease;
KW  Alzheimer's disease.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO9964587-A1.
XX
PD  16-DEC-1999.
XX
PF  04-JUN-1999; 99WO-FR001326.
XX
PR  05-JUN-1998; 98FR-00007068.
XX
PR  03-MAR-1999; 99US-0122599P.
XX
PA  (RHON ) RHONE-POULENC RORER SA.
PA  (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI  Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX
DR  WPI; 2000-097537/08.
XX
PD  16-DEC-1999.
XX
PF  04-JUN-1999; 99WO-FR001326.
XX
PR  05-JUN-1998; 98FR-00007068.
XX
PR  03-MAR-1999; 99US-0122599P.
XX
PA  (RHON ) RHONE-POULENC RORER SA.
PA  (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI  Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX
DR  WPI; 2000-097537/08.
XX
PT  Polypeptide with beta-secretase activity, specific for wild-type amyloid
PT  precursor protein, useful in treating Alzheimer's disease.
XX
PS  Example 3; Page 24; 44pp; French.
XX
CC  Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC  novel polypeptide with beta-secretase activity that can cleave
CC  specifically the natural beta-amyloid precursor protein (BAPP). Normal
CC  cleavage of the protein occurs between amino acids Met596-Asp597 and
CC  Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC  polypeptide is used to identify agents that interact specifically with
CC  it. These agents regulate metabolism of APP, particularly they slow down
CC  or reduce production of beta-amyloid, so can be used to treat
CC  neurodegenerative diseases, particularly Alzheimer's disease
XX
SQ  Sequence 10 AA;

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  VXXXXAEF 7
      |:::|
Db      3  VKIDAEF 9

RESULT 172
AAy69711
ID  AAY69711 standard; peptide; 10 AA.
AC  AAY69711;
XX
DT  11-APR-2000 (first entry)
XX

```

```

XX  DE  Beta-APP alpha-secretase substrate [XQN]-APP(-5,+5).
XX  KW  Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX  KW  cleavage site; beta-secretase; neurodegenerative disease;
XX  KW  Alzheimer's disease.
XX  OS  Homo sapiens.
XX  OS  Synthetic.
XX  PN  WO9964587-A1.
XX  XX
XX  PD  16-DEC-1999.
XX  XX
XX  PF  04-JUN-1999; 99WO-FR001326.
XX  XX
XX  PR  05-JUN-1998; 98FR-00007068.
XX  PR  03-MAR-1999; 99US-0122599P.
XX  XX
XX  PA  (RHON ) RHONE-POULENC RORER SA.
XX  PA  (UYPA-) UNIV CURIE PARIS VI P & M.
XX  XX
XX  PI  Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX  DR  WPI; 2000-097537/08.
XX  XX
XX  PT  Polypeptide with beta-secretase activity, specific for wild-type amyloid
XX  PT  precursor protein, useful in treating Alzheimer's disease.
XX  XX
XX  PS  Example 3; Page 24; 44pp; French.
XX  XX
XX  CC  Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
XX  CC  novel polypeptide with beta-secretase activity that can cleave
XX  CC  specifically the natural beta-amyloid precursor protein (BAPP). Normal
XX  CC  cleavage of the protein occurs between amino acids Met596-Asp597 and
XX  CC  Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
XX  CC  polypeptide is used to identify agents that interact specifically with
XX  CC  it. These agents regulate metabolism of APP, particularly they slow down
XX  CC  or reduce production of beta-amyloid, so can be used to treat
XX  CC  neurodegenerative diseases, particularly Alzheimer's disease
XX  SQ  Sequence 10 AA;

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  VXXXXAEF 7
      |:::|
Db      3  VKQNAEF 9

RESULT 173
AAy69712
ID  AAY69712 standard; peptide; 10 AA.
XX
AC  AAY69712;
XX
XX  DT  11-APR-2000 (first entry)
XX  XX
XX  DE  Beta-APP alpha-secretase substrate [XMQ]-APP(-5,+5).
XX  XX
XX  KW  Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX  KW  cleavage site; beta-secretase; neurodegenerative disease;
XX  KW  Alzheimer's disease.
XX  XX
XX  OS  Homo sapiens.
XX  OS  Synthetic.
XX  PN  WO9964587-A1.
XX  XX
XX  PD  16-DEC-1999.
XX  XX

```

```

PF 04-JUN-1999; 99WO-FR001326.
XX
PR 05-JUN-1998; 98FR-00007068.
PR 03-MAR-1999; 99US-0122599P.
XX
PA (RHON ) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
DR
XX
PT Polypeptide with beta-secretase activity, specific for wild-type amyloid
PT precursor protein, useful in treating Alzheimer's disease.
XX
PS Example 3; Page 24; 44pp; French.
XX
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 3 VKMQAEF 9
|:::|
|:::|

RESULT 174
AAY69703
ID AAY69703 standard; peptide; 10 AA.
XX
AC AAY69703;
XX
DT 11-APR-2000 (first entry)
XX
DE Beta-APP alpha-secretase substrate [RMD]-APP(-5,+5).
XX
KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW cleavage site; beta-secretase; neurodegenerative disease;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9964587-A1.
XX
PD 16-DEC-1999.
XX
PF 04-JUN-1999; 99WO-FR001326.
XX
PR 05-JUN-1998; 98FR-00007068.
PR 03-MAR-1999; 99US-0122599P.
XX
XX (RHON ) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
XX
DR
XX
PT Polypeptide with beta-secretase activity, specific for wild-type amyloid
PT precursor protein, useful in treating Alzheimer's disease.
XX
PS Example 3; Page 24; 44pp; French.
XX
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 3 VKMQAEF 9
|:::|
|:::|

RESULT 174
AAY69703
ID AAY69703 standard; peptide; 10 AA.
XX
AC AAY69703;
XX
DT 11-APR-2000 (first entry)
XX
DE Beta-APP alpha-secretase substrate [RMD]-APP(-5,+5).
XX
KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW cleavage site; beta-secretase; neurodegenerative disease;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9964587-A1.
XX
PD 16-DEC-1999.
XX
PF 04-JUN-1999; 99WO-FR001326.
XX
PR 05-JUN-1998; 98FR-00007068.
PR 03-MAR-1999; 99US-0122599P.
XX
XX (RHON ) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
XX
DR
XX
PT Polypeptide with beta-secretase activity, specific for wild-type amyloid
PT precursor protein, useful in treating Alzheimer's disease.
XX
PS Example 3; Page 24; 44pp; French.
XX
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
SQ Sequence 10 AA;

```

```

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
DB 3 VRMDAEF 9

RESULT 176
AAU07226
ID AAU07226 standard; peptide; 10 AA.
XX
AC AAU07226;
XX
XX 11-APR-2000 (first entry)
XX
DE Beta-APP alpha-secretase substrate [NMD]-APP(-5,+5).
XX
KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW cleavage site; beta-secretase; neurodegenerative disease;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9964587-A1.
XX
PD 16-DEC-1999.
XX
PF 04-JUN-1999; 99WO-FR001326.
XX
PR 05-JUN-1998; 98PR-00007068.
XX
PR 03-MAR-1999; 99US-0122599P.
XX
XX (RHON ) RHONE-POULENC RORER SA.
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type amyloid
PT precursor protein, useful in treating Alzheimer's disease.
XX
XX Example 3; Page 24; 44pp; French.
XX
XX Peptides AAU69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (BAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAU69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease
XX
XX Sequence 10 AA;
SQ

Query Match      100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
DB 3 VNMDAEF 9

RESULT 177
AAU07226
ID AAU07226 standard; peptide; 10 AA.
XX
XX AAU07226;
XX

XX 24-OCT-2001 (first entry)
XX
DE Human beta-amyloid protein precursor, APP-Sw beta-secretase site.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP-Sw.
XX
XX Homo sapiens.
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-502548/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
XX Claim 10; Page 84; 185pp; English.
XX
XX The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from APP nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human amyloid
CC protein precursor, APP-Sw, beta-secretase site
XX
XX Sequence 10 AA;
SQ

Query Match      100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
DB 3 VNLDAEF 9

RESULT 178
AAU07227
ID AAU07227 standard; peptide; 10 AA.
XX
XX

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AC AAU07227;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.
XX
XX Human, aspartyl protease 1; Asp-1; nontropic; neuroprotective;
XX aspartyl protease 2; Asp2; amyloid protein precursor; APP;
XX beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.
XX
XX Homo sapiens.
XX
XX WO200149097-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB000797.
XX
XX 09-MAY-2001; 2001WO-IB000797.
XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
XX WPI; 2001-502548/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Claim 127; Page 101; 185pp; English.
XX
XX The invention relates to a novel purified polypeptide comprising a
XX fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
XX Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
XX and the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. Also included is an isoform of amyloid protein precursor (APP)
XX comprising the amino acid sequence of a APP or its fragment containing an
XX APP cleavage site recognizable by a mammalian beta-secretase, and further
XX comprising two lysine residues at the carboxyl terminus of the amino acid
XX sequence of the mammalian APP or APP fragment. The polypeptides are used
XX for assaying for modulators of beta-secretase activity; identifying
XX agents that inhibit the APP processing activity of human Asp2 aspartyl
XX protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
XX ; and for reducing cellular production of amyloid beta (Abeta) from APP.
XX Agents identified by the above methods are useful for treating
XX Alzheimer's disease; and for identifying modulators of amyloid-beta
XX (Abeta) peptide production, for use in designing therapeutics for the
XX treatment or prevention of Alzheimer's disease. Probes and primers
XX derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
XX nucleic acids in vitro assays and in Northern and Southern blots. The
XX present sequence represents the amino acid sequence of human amyloid
XX protein precursor, APP-beta40 and APP-beta42 secretase sites
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 7; DB 4; Length 10;
XX Best Local Similarity 57.1%; Pred.No. 2.2e+02;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXXAEF 7
XX |:::|
XX Db 3 VKMDAEF 9
XX
XX RESULT 179
XX AA010653
XX ID AA010653 standard; peptide; 10 AA.

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```

XX
XX AA010653;
XX
XX 10-DEC-2001 (first entry)
XX
XX Human APP-Sw beta-secretase substrate peptide mutant, PHA-247574E.
XX
XX Human, aspartyl protease 1; Aspl; amyloid precursor protein;
XX Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective;
XX APP-Sw beta-secretase peptide; mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 4 /note= "Wild type Lys substituted with Asn"
XX Cleavage-site 5 .6
XX Misc-difference 5 /note= "Wild type Met substituted with Leu"
XX
XX GB2357767-A.
XX
XX 04-JUL-2001.
XX
XX 22-SEP-2000; 2000GB-00023315.
XX
XX 23-SEP-1999; 99US-00404133.
XX 23-SEP-1999; 99US-0155493P.
XX 23-SEP-1999; 99WO-US020881.
XX 13-OCT-1999; 99US-00416901.
XX 06-DEC-1999; 99US-0169232P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Bienkowski MJ, Gurney M;
XX
XX WPI; 2001-444208/48.
XX
XX Polypeptide comprising fragments of human aspartyl protease with amyloid
XX precursor protein processing activity and alpha-secretase activity, for
XX identifying modulators useful in treating Alzheimer's disease.
XX
XX Example 12; Page 84; 187pp; English.
XX
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl
XX proteins which lack transmembrane domain or amino terminal domain or
XX cytoplasmic domain and retains alpha-secretase activity and amyloid
XX protein precursor (APP) processing activity. The proteins of the
XX invention are useful for assaying hu-Aspl alpha-secretase activity, which
XX in turn is useful for identifying modulators of hu-Aspl alpha-secretase
XX activity, where modulators that increase hu-Aspl alpha-secretase activity
XX are useful for treating Alzheimer's disease (AD) which causes progressive
XX dementia with consequent formation of amyloid plaques, neurofibrillary
XX tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful
XX for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein
XX with the substrate under acidic conditions and determining the level of
XX hu-Aspl proteolytic activity. The present sequence is human amyloid
XX precursor protein-Swedish (APP-Sw) beta-secretase specific Swedish KM-NL
XX peptide mutant, PHA-247574E. This peptide is obtained by Swedish KM-NL
XX mutation. This peptide is used for assaying the beta-secretase activity
XX of human Aspartyl protease 2a (Asp2a) protein. The peptide is also used
XX for determining the relationship between Aspl and APP protein
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 7; DB 4; Length 10;
XX Best Local Similarity 57.1%; Pred.No. 2.2e+02;
XX Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VXXXXAEF 7
XX |:::|

```

Db 3 VNLDAEF 9

RESULT 180
AAE10654
ID AAE10654 standard; peptide; 10 AA.
XX AAE10654;
AC
XX
DT 10-DEC-2001 (first entry)
XX
DE Human wild-type APP beta-secretase peptide, PHA-95812E.
XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;
KW APP beta-secretase peptide.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5..6
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
XX
XX Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Example 12; Page 84; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is wild-type human
CC amyloid precursor protein (APP) beta-secretase specific substrate
CC peptide, PHA-95812E. This peptide is used for assaying the beta-secretase
CC activity of human Aspartyl protease 2a (Asp2a) protein. The peptide is
CC also used for determining the relationship between Aspartyl protease 1
CC (Asp1) and APP protein
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7

Db 3 VNMDAEF 9

RESULT 181
AAE06899
ID AAE06899 standard; peptide; 10 AA.
XX AAE06899;
AC
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein wild-type beta-secretase peptide.
XX
KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW neuroprotective; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5..6
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Claim 127; Page 80; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. App isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is human amyloid precursor protein (APP) wild type
CC beta-secretase peptide used in beta-secretase assay
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. NO. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 182

AAE06898
ID AAE06898 standard; peptide; 10 AA.

XX AC AAE06898;

XX DT 23-OCT-2001 (first entry)

XX DE Human amyloid precursor protein (APP-Sw) beta-secretase peptide #1.

XX DE Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW neuroprotective; antisense therapy; APP-Sw; gene therapy.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers
XX FT Cleavage-site 5..6

XX PN WO200150829-A2.

XX PD 19-JUL-2001.

XX PF 09-MAY-2001; 2001WO-IB000799.

XX PR 09-MAY-2001; 2001WO-IB000799.

XX PA (BIEN/) BIENKOWSKI M J.

XX PA (GURN/) GURNEY M E.

XX PA (HEIN/) HEINRIKSON R L.

XX PA (PARO/) PARODI L A.

XX PA (YANR/) YAN R.

XX PI Bienkowski MJ, Gurney ME, Heinriksen RL, Parodi LA, Yan R;

XX DR WPI; 2001-483072/52.

XX PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX PS Claim 10; Page 84; 185pp; English.

XX CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC APP nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is human amyloid precursor protein (APP-Sw) beta-
CC secretase peptide related to the invention

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 183

AAE46208
ID AAE46208 standard; peptide; 10 AA.

XX AC AAE46208;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #4.

XX DE Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX DR WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (FC
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 184

AAE46207
ID AAE46207 standard; peptide; 10 AA.

XX AC AAE46207;

XX XX

```

DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #3.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.
XX
PS Disclosure; Fig 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
1 VKMDAEF 7

RESULT 185
AAB46210
ID AAB46210 standard; peptide; 10 AA.
XX
AC AAB46210;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #6.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX

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PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.
XX
PS Disclosure; Fig 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db |::|||
1 VKMDAEF 7

RESULT 186
AAB46209
ID AAB46209 standard; peptide; 10 AA.
XX
AC AAB46209;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #5.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX WPI; 2001-032104/04.
XX

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PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid specific
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |:::|
 Db 2 VKMDAEP 8

RESULT 187

AAB61337
 ID AAB61337 standard; peptide; 10 AA.

XX AC AAB61337;

XX DT 02-APR-2001 (first entry)

XX DE Swedish mutation peptide from beta amyloid precursor protein.

XX KW Memapsin 2; catalyst; Alzheimer's.

XX OS Unidentified.

XX PN WO200100663-A2.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-US017661.

XX PR 28-JUN-1999; 99US-0141363P.

XX PR 30-NOV-1999; 99US-0168060P.

XX PR 25-JAN-2000; 2000US-0177836P.

XX PR 27-JAN-2000; 2000US-0178368P.

XX PR 08-JUN-2000; 2000US-0210292P.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Tang JJN, Lin X, Koelsch G;

XX DR WPI; 2001-102885/11.

XX PT Purified recombinant catalytically active memapsin 2, used to screen

XX PT inhibitors of it, which are used to treat and prevent Alzheimer's

XX PT disease.

XX PS Claim 6; Page 11; 86pp; English.

XX CC The present invention relates to a purified recombinant catalytically

XX CC active memapsin 2. The invention may be used for isolating inhibitors

XX CC which are used to treat or prevent Alzheimer's disease. The invention may

XX CC also be used to screen for individuals more genetically prone to develop

CC Alzheimer's disease
 XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |:::|
 Db 3 VKMDAEP 9

RESULT 188

AAB61336
 ID AAB61336 standard; peptide; 10 AA.

XX AC AAB61336;

XX DT 02-APR-2001 (first entry)

XX DE Synthetic peptide from beta amyloid precursor protein.

XX KW Memapsin 2; catalyst; Alzheimer's.

XX OS Unidentified.

XX PN WO200100663-A2.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-US017661.

XX PR 28-JUN-1999; 99US-0141363P.

XX PR 30-NOV-1999; 99US-0168060P.

XX PR 25-JAN-2000; 2000US-0177836P.

XX PR 27-JAN-2000; 2000US-0178368P.

XX PR 08-JUN-2000; 2000US-0210292P.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Tang JJN, Lin X, Koelsch G;

XX DR WPI; 2001-102885/11.

XX PT Purified recombinant catalytically active memapsin 2, used to screen

XX PT inhibitors of it, which are used to treat and prevent Alzheimer's

XX PT disease.

XX PS Claim 6; Page 11; 86pp; English.

XX CC The present invention relates to a purified recombinant catalytically

XX CC active memapsin 2. The invention may be used for isolating inhibitors

XX CC which are used to treat or prevent Alzheimer's disease. The invention may

XX CC also be used to screen for individuals more genetically prone to develop

XX CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |:::|
 Db 3 VKMDAEP 9

RESULT 189

AAE02605
 ID AAE02605 standard; peptide; 10 AA.

XX AC AAE02605;

```

XX DT 10-AUG-2001 (first entry)
XX DE Human App-Sw beta-secretase substrate peptide mutant, PHA-247574E.
XX KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
XX KW beta-secretase; mutant; muten.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 4
XX FT /note= "Wild type Lys substituted with Asn"
XX FT Cleavage-site 5..6
XX FT Misc-difference 5
XX FT /note= "Wild type Met substituted with Leu"
XX FT
XX PN WO200123533-A2.
XX PD
XX PD 05-APR-2001.
XX PF
XX PF 22-SEP-2000; 2000WO-US026080.
XX PR
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI
XX PI Gurney M, Bienkowski MJ;
XX DR WPI; 2001-290516/30.
XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease.
XX PS Example 12; Page 85; 189pp; English.
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human amyloid precursor
XX CC protein (APP)-Swedish (Sw) beta-secretase specific substrate peptide
XX CC mutant, PHA-247574E. This peptide is obtained by Swedish KM-NL mutation.
XX CC The peptide is used for assaying the beta-secretase activity of human
XX CC Aspartyl protease 2a (Asp2a) protein. The peptide is also used for
XX CC determining the relationship between Aspartyl protease 1 (Asp1) and APP
XX CC protein
XX SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
Db 3 VNLDAEF 9

RESULT 190
AAE02606
ID AAE02606 standard; peptide; 10 AA.
XX AC
XX AC AAE02606;
XX DT
XX DT 10-AUG-2001 (first entry)
XX DE Human wild-type APP beta-secretase substrate peptide, PHA-95812E.

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XX KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
XX KW beta-secretase.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Cleavage-site 5..6
XX PN WO200123533-A2.
XX PD
XX PD 05-APR-2001.
XX PF
XX PF 22-SEP-2000; 2000WO-US026080.
XX PR
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI
XX PI Gurney M, Bienkowski MJ;
XX DR WPI; 2001-290516/30.
XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease.
XX PS Example 12; Page 85; 189pp; English.
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human wild-type amyloid
XX CC precursor protein (APP) beta-secretase specific substrate peptide, PHA-
XX CC 95812E. This peptide is used for assaying the beta-secretase activity of
XX CC human Aspartyl protease 2a (Asp2a) protein. The peptide is also used for
XX CC determining the relationship between Aspartyl protease 1 (Asp1) and APP
XX CC protein
XX SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
Db 3 VKMDAEF 9

RESULT 191
AAB66574
ID AAB66574 standard; peptide; 10 AA.
XX AC
XX AC AAB66574;
XX DT
XX DT 12-APR-2001 (first entry)
XX DE Synthetic peptide derived from APP beta-secretase site.
XX KW Memapsin 2; nootropic; neuroprotective; amyloid precursor protein; APP;
XX KW memapsin 2 inhibitor; Alzheimer's disease.
XX OS Synthetic.
XX PN WO200100665-A2.
XX PD
XX PD 04-JAN-2001.

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XX PF 27-JUN-2000; 2000WO-US017742.
XX PR 28-JUN-1999; 99US-0141363P.
XX PR 30-NOV-1999; 99US-0168060P.
XX PR 25-JAN-2000; 2000US-0177836P.
XX PR 27-JAN-2000; 2000US-0178368P.
XX PR 08-JUN-2000; 2000US-0210292P.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PA (UNII ) UNIV ILLINOIS FOUND.
XX PI Tang JJN, Hong L, Ghosh AK;
XX DR WPI; 2001-137933/14.
XX PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
XX PT having 2 catalytic aspartic residues and substrate binding cleft, used to
XX PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.
XX PS Disclosure; Page 11; 86pp; English.
XX CC The present sequence is given in a specification relating to an inhibitor
XX CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
XX CC active site, which is defined by the presence of two catalytic aspartic
XX CC residues and a substrate binding cleft. The inhibitor is useful for the
XX CC treatment and diagnosis of Alzheimer's disease. It is useful in screens
XX CC for individuals with a genetic predisposition to Alzheimer's disease. The
XX CC inhibitor is useful as a reagent for specifically binding to memapsin 2
XX CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,
XX CC purification and characterisation
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 3 VKWDADF 9
|::|||

RESULT 192
AAB66575
ID AAB66575 standard; peptide; 10 AA.
XX AC AAB66575;
XX DT 12-APR-2001 (first entry)
XX DE Synthetic peptide derived from APP beta-secretase site.
XX KW Memapsin 2; neurotropic; neuroprotective; amyloid precursor protein; APP;
XX KW memapsin 2 inhibitor; Alzheimer's disease.
XX OS Synthetic.
XX PN WO200100665-A2.
XX PD 04-JAN-2001.
XX PF 27-JUN-2000; 2000WO-US017742.
XX PR 28-JUN-1999; 99US-0141363P.
XX PR 30-NOV-1999; 99US-0168060P.
XX PR 25-JAN-2000; 2000US-0177836P.
XX PR 27-JAN-2000; 2000US-0178368P.
XX PR 08-JUN-2000; 2000US-0210292P.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PA (UNII ) UNIV ILLINOIS FOUND.
XX

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PI Tang JJN, Hong L, Ghosh AK;
XX DR WPI; 2001-137933/14.
XX PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
XX PT having 2 catalytic aspartic residues and substrate binding cleft, used to
XX PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.
XX PS Disclosure; Page 11; 86pp; English.
XX CC The present sequence is given in a specification relating to an inhibitor
XX CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
XX CC active site, which is defined by the presence of two catalytic aspartic
XX CC residues and a substrate binding cleft. The inhibitor is useful for the
XX CC treatment and diagnosis of Alzheimer's disease. It is useful in screens
XX CC for individuals with a genetic predisposition to Alzheimer's disease. The
XX CC inhibitor is useful as a reagent for specifically binding to memapsin 2
XX CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,
XX CC purification and characterisation
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 3 VNLDAEF 9
|::|||

RESULT 193
AAG62668
ID AAG62668 standard; peptide; 10 AA.
XX AC AAG62668;
XX DT 17-SEP-2001 (first entry)
XX DE Beta-sheet breaker peptide inhibitor assay related peptide #3.
XX KW Beta-sheet breaker peptide; protein conformational disease; amyloid;
XX KW Alzheimer's disease; FAF; Down, syndrome; amyloidosis disorder;
XX KW prion disease; prion associated neurodegenerative disease.
XX OS Synthetic.
XX PN WO200134631-A2.
XX PD 17-MAY-2001.
XX PF 04-NOV-2000; 2000WO-US030416.
XX PR 05-NOV-1999; 99US-0163911P.
XX PA (AXON-) AXONYX INC.
XX PI Soto-Jara C;
XX DR WPI; 2001-408068/43.
XX PT New peptide analogues and mimetics, useful by oral administration for the
XX PT treatment of Alzheimer's and prion disease by stabilization of the
XX PT conformation of amyloidogenic peptide.
XX PS Example; Page 28; 48pp; English.
XX CC The present invention relates to beta-sheet breaker peptide analogues
XX CC capable of inhibiting beta-pleated sheet formation in amyloid beta-
XX CC peptide. These are obtained by modification of a beta-sheet breaker
XX CC peptide. They can be used to reduce the formation of amyloid or amyloid-
XX CC like deposits involving abnormal folding into beta-sheet structures or
XX CC conformational change in prion Pr protein. They are thus useful in the

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CC treatment of Alzheimer's disease, FAF, Down's syndrome, other amyloidosis
CC disorders, prion diseases such as kuru, Creutzfeldt-Jakob disease,
CC Gerstmann-Strauslet-Scheinker syndrome, prion associated human
CC neurodegenerative diseases, scrapie, spongiform encephalopathy,
CC transmissible mink encephalopathy and chronic wasting disease of mule
CC deer and elk. The present sequence is a peptide described in the
CC exemplification of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 4 VKWDAEF 10

RESULT 194
AAB47266
ID AAB47266 standard; peptide; 10 AA.
XX
AC AAB47266;

XX 18-JUL-2001 (first entry)
XX Peptide 5-5'SW, for used in beta-secretase assay.

XX Beta-secretase; isotype; beta-amyloid precursor protein; APP;
KW beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.

XX Synthetic.
XX US6221645-B1.

XX 24-APR-2001.

XX 07-JUN-1996; 96US-00660531.

XX 07-JUN-1995; 95US-00480498.

XX (ELAN-) ELAN PHARM INC.

XX Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H;

XX Mcconlogue LC;

XX WPI; 2001-315578/33.

XX Novel antibody that specifically binds native beta-secretase protein,
PT useful for raising anti-idiotypic antibodies and for detecting or
PT diagnosing pathological conditions related to presence of respective
PT antigens.

XX Example; Col 30; 42pp; English.

XX The sequences given in AAB47262-67 represent synthetic peptides
CC containing the cleavage sites derived from wild-type beta-amyloid
CC precursor protein (APP). These peptides were used in assays utilising
CC partially purified beta-secretase to identify beta-secretase inhibitors.
CC Beta-secretase is thought to be responsible for the pathogenic processing
CC of APP to form beta amyloid peptide (beta-AP) in beta-AP related
CC conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D etc. Beta-
CC secretase has a molecular weight of 260-300 kD and will bind to wheat
CC germ agglutinin but not to concanavalin A. Beta-secretase will cleave
CC both the wild type and the Swedish mutation of APP

XX Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VNLDAEF 9

RESULT 195

AAU06627
ID AAU06627 standard; peptide; 10 AA.

XX AAU06627;

XX 24-OCT-2001 (first entry)

XX Synthetic Asp2 recognition site from APP-SW.

XX Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;
KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta;
KW APP-SW.

XX Synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 5
FT /label= Asp2_protease_cleavage_site

XX WO200149098-A2.

XX 12-JUL-2001.

XX 09-MAY-2001; 2001WO-IB000798.

XX 09-MAY-2001; 2001WO-IB000798.

XX (BIEN/) BIENKOWSKI M J.

XX (GURN/) GURNEY M E.

XX (HEIN/) HEINRIKSON R L.

XX (PARO/) PARODI L A.

XX (YANR/) YAN R.

XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX WPI; 2001-502549/55.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX Claim 10; Page 84; 185pp; English.

XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or
CC its fragment containing an APP cleavage site recognizable by a mammalian
CC beta-secretase, and further comprising two lysine residues at the
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC comprising the APP-SW-beta-secretase peptide sequence (NLDA), which is
CC associated with increased levels of Abeta processing is useful in assays
CC relating the Alzheimer's research. The expression vector is useful for
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC oligonucleotides are useful as probes or primers. The probes are useful
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and

CC Southern blots. The present sequence is an synthetic peptide substrate
 CC for Asp2 corresponding to the App swedish mutation site, APP-SW
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |:::|
 Db 3 VNLDAEF 9

RESULT 196
 AAU06628
 ID AAU06628 standard; peptide; 10 AA.
 XX AC AAU06628;
 DT 24-OCT-2001 (first entry)
 DE Asp2 recognition site from wild-type APP.
 XX
 KW Aspartyl protease; Asp2; beta-secretase; nontropic; neuroprotective;
 KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5 /label= Asp2_protease_cleavage_site
 XX WO200149098-A2.
 XX 12-JUL-2001.
 XX
 XX 09-MAY-2001; 2001WO-IB000798.
 XX
 XX 09-MAY-2001; 2001WO-IB000798.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURN/) GURNEY M E.
 XX (HEIN/) HEINRIKSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI; 2001-502549/55.
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity..
 XX
 XX Claim 127; Page 101; 185pp; English.
 XX

CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp proteins
 CC and vectors expressing them, and a polypeptide (isoform of amyloid
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or
 CC its fragment containing an APP cleavage site recognizable by a mammalian
 CC beta-secretase, and further comprising two lysine residues at the
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
 CC fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing

CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the App-Sw-beta-secretase peptide sequence (NLDA), which is
 CC associated with increased levels of Abeta expression is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridize to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is a peptide substrate for Asp2
 CC corresponding to the wild-type APP beta-secretase site
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 7; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |:::|
 Db 3 VVMDAEF 9

RESULT 197
 ABB06426
 ID ABB06426 standard; peptide; 10 AA.
 XX AC ABB06426;
 DT 31-MAY-2002 (first entry)
 XX
 DE Human APP beta-secretase cleavage sequence SEQ ID NO:20.
 XX
 KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KW aspartyl protease; neuroprotective; nontropic; beta-secretase inhibitor;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200206306-A2.
 XX 24-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US023035.
 XX
 XX 19-JUL-2000; 2000US-0219795P.
 XX 12-MAR-2001; 2001US-0275251P.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 XX Heinrikson RL;
 XX WPI; 2002-216995/27.
 XX
 XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease.
 XX
 XX Claim 18; Page 126; 188pp; English.
 XX

CC The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nontropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
 CC a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification of
 CC the present invention

```

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|
DB 3 VNXDAEF 9

RESULT 198
ABB06427
ID ABB06427 standard; peptide; 10 AA.
XX
AC ABB06427;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human APP Swedish KM-NL mutation beta-secretase cleavage sequence SEQ:19.
XX
KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200206306-A2.
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US023035.
XX
PR 19-JUL-2000; 2000US-0219795P.
PR 12-MAR-2001; 2001US-0275251P.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
WPI; 2002-216995/27.
XX
PT Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease.
XX
PS Claim 19; Page 84; 188pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
CC a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|
DB 3 VNXDAEF 9

RESULT 200
ABB06548
ID ABB06548 standard; peptide; 10 AA.
XX

```

```

AC ABB06548;
XX
XX
DT 31-MAY-2002 (first entry)
XX
XX DE Beta-secretase cleavage site peptide SEQ ID NO:143.
XX
XX DE Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
XX KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
XX KW Alzheimer's disease.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200206306-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 19-JUL-2001; 2001WO-US023035.
XX
XX PR 19-JUL-2000; 2000US-0219795P.
XX PR 12-MAR-2001; 2001US-0275251P.
XX
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
XX PI Heinrikson RL;
XX
XX DR WPI; 2002-216995/27.
XX
XX PT Novel substrates for human aspartyl protease useful for identifying
XX PT modulators of beta secretase activity of aspartyl protease for treating
XX PT Alzheimer's disease.
XX
XX PS Claim 20; Page 169; 188pp; English.
XX
XX CC The present invention describes an isolated peptide (I) comprising a
XX CC sequence of at least four amino acids, where the peptide is a substrate
XX CC for conducting aspartyl protease assays. (I) has neuroprotective and
XX CC nootropic activities, and can be used as an inhibitor of beta-secretase
XX CC activity. A beta-secretase modulator from the present invention can be
XX CC used for inhibiting beta-secretase activity in vivo, and in the
XX CC manufacture of a medicament for the treatment of Alzheimer's disease.
XX CC Pharmaceutical compositions from the present invention can be used for
XX CC treating a disease or condition characterised by an abnormal beta-
XX CC secretase activity. (I) is useful for identifying agents that modulate
XX CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
XX CC a core structure to construct derivatives. ABL49914 to ABL49925 and
XX CC ABB06409 to ABB06593 represent sequences used in the exemplification of
XX CC the present invention
XX
XX SQ Sequence 10 AA;

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Query Match      100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VXXXAEEF 7
Db 3 VSYDAEF 9

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Job time : 128.5 secs

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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:30 ; Search time 29.5 Seconds
(without alignments)
17.713 Million cell updates/sec

Title: SEQ59

Perfect score: 7

Sequence: 1 vxxxaef 7

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

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Total number of hits satisfying chosen parameters: 896

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
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- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	2	US-08-792-553-10
2	7	100.0	7	4	US-09-129-192C-44
3	7	100.0	7	4	US-09-604-608-27
4	7	100.0	7	4	US-09-724-566A-78
5	7	100.0	7	4	US-08-594-575C-10
6	7	100.0	7	4	US-09-471-669A-78
7	7	100.0	8	4	US-09-548-372D-67
8	7	100.0	8	4	US-09-548-367D-67
9	7	100.0	8	4	US-09-551-853D-67
10	7	100.0	8	4	US-09-604-608-28
11	7	100.0	8	4	US-09-724-566A-81
12	7	100.0	8	4	US-09-416-901B-67
13	7	100.0	8	4	US-09-548-376D-67
14	7	100.0	8	4	US-09-794-927A-67
15	7	100.0	8	4	US-09-548-373D-67
16	7	100.0	8	4	US-09-795-847B-67
17	7	100.0	8	4	US-09-869-414-67
18	7	100.0	8	4	US-09-548-366F-67
19	7	100.0	8	4	US-09-548-368D-67
20	7	100.0	8	4	US-09-794-925A-67
21	7	100.0	8	4	US-09-471-669A-81
22	7	100.0	9	3	US-08-802-981-219
23	7	100.0	9	3	US-08-802-981-220
24	7	100.0	9	3	US-08-802-981-221
25	7	100.0	9	3	US-09-294-987-6
26	7	100.0	9	4	US-09-724-566A-52
27	7	100.0	9	4	US-09-724-566A-73

28 7 100.0 9 4 US-09-724-566A-82 Sequence 82, Appl
29 7 100.0 9 4 US-09-724-566A-83 Sequence 83, Appl
30 7 100.0 9 4 US-09-724-566A-84 Sequence 84, Appl
31 7 100.0 9 4 US-09-724-566A-85 Sequence 85, Appl
32 7 100.0 9 4 US-09-724-566A-86 Sequence 86, Appl
33 7 100.0 9 4 US-09-724-566A-87 Sequence 87, Appl
34 7 100.0 9 4 US-09-724-566A-88 Sequence 88, Appl
35 7 100.0 9 4 US-09-724-566A-89 Sequence 89, Appl
36 7 100.0 9 4 US-09-724-566A-90 Sequence 90, Appl
37 7 100.0 9 4 US-09-724-566A-91 Sequence 91, Appl
38 7 100.0 9 4 US-09-724-566A-92 Sequence 92, Appl
39 7 100.0 9 4 US-09-724-566A-93 Sequence 93, Appl
40 7 100.0 9 4 US-09-724-566A-94 Sequence 94, Appl
41 7 100.0 9 4 US-09-724-566A-95 Sequence 95, Appl
42 7 100.0 9 4 US-09-724-566A-96 Sequence 96, Appl
43 7 100.0 9 4 US-09-471-669A-52 Sequence 52, Appl
44 7 100.0 9 4 US-09-471-669A-73 Sequence 73, Appl
45 7 100.0 9 4 US-09-471-669A-82 Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-08-792-553-10
; Sequence 10, Application US/08792553
; Patent No. 5981200
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Heim, Roger
; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,553
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-792-553-10

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7

Db 1 VKMDAEF 7

```
RESULT 2
US-09-129-192C-44
; Sequence 44, Application US/09129192C
; Patent No. 6495664
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; APPLICANT: Cubitt, Andrew B.
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AU01270 (08366/031001)
; CURRENT APPLICATION NUMBER: US/09/129,192C
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: b-Secretase for amyloid precursor protein
US-09-129-192C-44

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      ||::|||
Db      1 VRMDAEF 7

RESULT 3
US-09-604-608-27
; Sequence 27, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xianli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-604-608-27

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      ||::|||
Db      1 VNLAAEF 7

RESULT 4
US-09-724-566A-78
; Sequence 78, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guricbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-78

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      ||::|||
Db      1 VMKVAEF 7

RESULT 5
US-08-594-575C-10
; Sequence 10, Application US/08594575C
; Patent No. 6803188
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Heim, Roger
; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,575C
; FILING DATE: 31-JAN-1996
```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D..
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/030001/UC 96-160-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-594-575C-10

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
DB 1 VKMDAEF 7

RESULT 6
US-09-471-669A-78
; Sequence 78, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; FEATURE:
; OTHER INFORMATION: inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-471-669A-78

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7

Db 1 VMXVAEEF 7
|:::|

RESULT 7
US-09-548-372D-67
; Sequence 67, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-372D-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
DB 2 VKMDAEF 8

RESULT 8
US-09-548-367D-67
; Sequence 67, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-367D-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;

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Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VKWDAEF 8

RESULT 9
US-09-551-853D-67
; Sequence 67, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-551-853D-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VKWDAEF 8

RESULT 10
US-09-604-608-28
; Sequence 28, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-604-608-28

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VNLADEF 8

RESULT 11
US-09-724-566A-81
; Sequence 81, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varchese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-81

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VMKVAEF 8

RESULT 12
US-09-416-901B-67
; Sequence 67, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280A
```


; CURRENT APPLICATION NUMBER: US/09/416,901B
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-416-901B-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 13

US-09-548-376D-67
; Sequence 67, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-376D-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 14

US-09-794-927A-67
; Sequence 67, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:

; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-794-927A-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 15

US-09-548-373D-67
; Sequence 67, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280B
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-373D-67

Query Match 100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

```
RESULT 16
US-09-795-847B-67
; Sequence 67, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Farodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-795-847B-67

Query Match          100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 17
US-09-869-414-67
; Sequence 67, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-869-414-67

Query Match          100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 18
US-09-548-366F-67
; Sequence 67, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280U
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-548-366F-67

Query Match          100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 19
US-09-548-368D-67
; Sequence 67, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/548,368D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-368D-67

Query Match      100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 20
US-09-794-925A-67
; Sequence 67, Application US/09794925A
; Patent No. 6828117
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-794-925A-67

Query Match      100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 21
US-09-471-669A-81
; Sequence 81, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
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; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: Inhibitor P4-P4' XD-V
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)
; OTHER INFORMATION: Xaa is hydroxyethylene or statine.
; US-09-471-669A-81

Query Match      100.0%; Score 7; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VMXVAEF 8

RESULT 22
US-08-802-981-219
; Sequence 219, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-802-981-219
```

```
Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9

RESULT 23
US-08-802-981-220
; Sequence 220, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-220

Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9

RESULT 24
US-08-802-981-221
; Sequence 221, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
```

```
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-221

Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 25
US-09-294-987-6
; Sequence 6, Application US/09294987
; Patent No. 6313288
; GENERAL INFORMATION:
; APPLICANT: Hook, Vivian Y.H.
; TITLE OF INVENTION: SECTASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE: P-AS 3515
; CURRENT APPLICATION NUMBER: US/09/294,987
; CURRENT FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: US 09/173,887
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mammalian
US-09-294-987-6

Query Match 100.0%; Score 7; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 26
US-09-724-566A-52
; Sequence 52, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/724,566A
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-52
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VNLDAEF 9
```

```
RESULT 27
US-09-724-566A-73
; Sequence 73, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/724,566A
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P4-P4'stad-V peptide inhibitor
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Xaa is statine moiety
US-09-724-566A-73
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VNXVAEF 9
```

```
RESULT 28
US-09-724-566A-82
; Sequence 82, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/724,566A
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-09-724-566A-82
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VKMDAEF 9
```

```
RESULT 29
US-09-724-566A-83
; Sequence 83, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
```

```
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
; US-09-724-566A-83
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
Db 3 VKLDAEEF 9
```

```
RESULT 30
US-09-724-566A-84
; Sequence 84, Application US/09724566A
; Patent No. 6627739
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-09-724-566A-84
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
Db 3 VKLDAEEF 9
```

```
RESULT 31
US-09-724-566A-85
; Sequence 85, Application US/09724566A
; Patent No. 6627739
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-09-724-566A-85
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
Db 3 VKLDAEEF 9
```

```
RESULT 32
US-09-724-566A-86
; Sequence 86, Application US/09724566A
; Patent No. 6627739
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
```

```
/ TITLE OF INVENTION: Methods
/ FILE REFERENCE: 228-US-NEWC2
/ CURRENT APPLICATION NUMBER: US/09/724,566A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 86
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: APP fragment
US-09-724-566A-86
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VNFDAEF 9
|:::|
```

```
RESULT 33
US-09-724-566A-87
/ Sequence 87, Application US/09724566A
/ Patent No. 6627739
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basi, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, No. 6627739mand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEWC2
/ CURRENT APPLICATION NUMBER: US/09/724,566A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 87
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: APP fragment
US-09-724-566A-87
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VKMAAEF 9
|:::|
```

```
RESULT 34
US-09-724-566A-88
/ Sequence 88, Application US/09724566A
/ Patent No. 6627739
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basi, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, No. 6627739mand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEWC2
/ CURRENT APPLICATION NUMBER: US/09/724,566A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 88
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: APP fragment
US-09-724-566A-88
```

```
Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VNLAAEF 9
|:::|
```

```
RESULT 35
US-09-724-566A-89
/ Sequence 89, Application US/09724566A
/ Patent No. 6627739
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basi, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, No. 6627739mand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEWC2
/ CURRENT APPLICATION NUMBER: US/09/724,566A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
```

```

; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-09-724-566A-89

```

```

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VKLAEEF 9

```

RESULT 36

```

US-09-724-566A-90
; Sequence 90, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-09-724-566A-90

```

```

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VKMLAEF 9

```

RESULT 37

```

US-09-724-566A-91
; Sequence 91, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.

```

```

; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-09-724-566A-91

```

```

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VNLLAEF 9

```

RESULT 38

```

US-09-724-566A-92
; Sequence 92, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: APP fragment
US-09-724-566A-92

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 3 VKLLAEF 9

RESULT 39

US-09-724-566A-93
; Sequence 93, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; FILE REFERENCE: 228-US-NEWC2

; CURRENT APPLICATION NUMBER: US/09/724,566A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 93

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: APP fragment

US-09-724-566A-93

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 3 VKFAAEF 9

RESULT 40

US-09-724-566A-94

; Sequence 94, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

QY 1 VXXAAEF 7
|:::|
Db 3 VNFLAEF 9

RESULT 42

US-09-724-566A-96
; Sequence 96, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-09-724-566A-96

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 3 VNFLAEF 9

RESULT 43

US-09-724-566A-52
; Sequence 52, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408

; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligopeptide substrate
US-09-471-669A-52

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 3 VNFLAEF 9

RESULT 44

US-09-471-669A-73
; Sequence 73, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P4-P4'stad-V
; OTHER INFORMATION: peptide inhibitor
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Xaa is statine moiety
US-09-471-669A-73

Query Match 100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|

```
Db          3 VNXVABF 9

RESULT 45
US-09-471-669A-82
; Sequence 82, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-82

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VXXXAEF 7
           |:::|||
Db          3 VNLDAEF 9

RESULT 46
US-09-471-669A-83
; Sequence 83, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-83

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VXXXAEF 7
           |:::|||
Db          3 VXXDAEF 9

RESULT 47
US-09-471-669A-84
; Sequence 84, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-84

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VXXXAEF 7
           |:::|||
Db          3 VNLDAEF 9

RESULT 48
US-09-471-669A-85
; Sequence 85, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
```

```
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-85

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.le+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXXAEF 7
Db      3 VXFDAEF 9

RESULT 49
US-09-471-669A-86
; Sequence 86, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-86
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; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-86

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.le+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXXAEF 7
Db      3 VNFDAEF 9

RESULT 50
US-09-471-669A-87
; Sequence 87, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-87

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.le+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXXAEF 7
Db      3 VXXAAEF 9

RESULT 51
US-09-471-669A-88
; Sequence 88, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
```

```

; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-88

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VNLAAEF 9

RESULT 52
US-09-471-669A-89
; Sequence 89, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-89

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VNLAAEF 9

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Db      3 VKLAAEF 9

RESULT 53
US-09-471-669A-90
; Sequence 90, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-90

Query Match      100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VKLAAEF 9

RESULT 54
US-09-471-669A-91
; Sequence 91, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31

```

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; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-91

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLLAEF 9

RESULT 55
US-09-471-669A-92
; Sequence 92, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-93

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKFAAEF 9

RESULT 57
US-09-471-669A-94
; Sequence 94, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-92

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLLAEF 9

RESULT 56
US-09-471-669A-93
; Sequence 93, Application US/09471669A
; Patent No. 6830918

```

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-93

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKFAAEF 9

RESULT 57
US-09-471-669A-94
; Sequence 94, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-94

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
Db       3 VNFAEF 9

RESULT 58
US-09-471-669A-95
; Sequence 95, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribail
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-95

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
Db       3 VNFAEF 9

RESULT 59
US-09-471-669A-96
; Sequence 96, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribail
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
```

```
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-96

Query Match          100.0%; Score 7; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
Db       3 VNFAEF 9

RESULT 60
US-07-766-351-1
; Sequence 1, Application US/07766351
; Patent No. 5292652
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,351
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
```

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/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /label= Xaa4
/ OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 5
/ OTHER INFORMATION: /label= Xaa5
/ OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-07-766-351-1
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```
Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXAAEF 7
Db 3 VXXDAEF 9
```

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RESULT 61
US-08-059-032-1
; Sequence 1, Application US/08059032
; Patent No. 5424205
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower,
; STREET: Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,032
; FILING DATE: 19930507
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William E.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
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/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /label= Xaa4
/ OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 5
/ OTHER INFORMATION: /label= Xaa5
/ OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-08-059-032-1
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```
Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXAAEF 7
Db 3 VXXDAEF 9
```

```
RESULT 62
US-08-025-321C-1
; Sequence 1, Application US/08025321C
; Patent No. 5849560
; GENERAL INFORMATION:
; APPLICANT: Abraham Ph.D., Carmela R.
; TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGRADATION
; TITLE OF INVENTION: OF AMYLOID BETA-PROTEIN PRECURSOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/025,321C
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0079571-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 248 5000
; TELEFAX: 617 248 4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-025-321C-1
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```
Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VXXAAEF 7
Db 4 VKMDAEF 10
```

```
RESULT 63
US-08-659-984A-19
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```
; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
; US-08-659-984A-19

Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 64
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
```

```
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
; US-08-660-531-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 65
US-09-548-372D-63
; Sequence 63, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-09-548-372D-63

Query Match 100.0%; Score 7; DB 4; Length 10;
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```
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9

RESULT 66
US-09-548-372D-64
; Sequence 64, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAAEF 9

RESULT 67
US-09-548-367D-63
; Sequence 63, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
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```
US-09-548-367D-63

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9

RESULT 68
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAAEF 9

RESULT 69
US-09-551-853D-63
; Sequence 63, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-551-853D-63

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VKMDAEF 9

RESULT 70

US-09-551-853D-64
; Sequence 64, Application US/09551853D
; Patent No. 650667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551.853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-551-853D-64

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VKMDAEF 9

RESULT 71

US-09-604-608-4
; Sequence 4, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-604-608-4

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VKMDAEF 9

RESULT 72

US-09-604-608-5
; Sequence 5, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-604-608-5

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VKMDAEF 9

RESULT 73

US-09-416-901B-63
; Sequence 63, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280A
; FILE REFERENCE: 29915/6280A

```
/ CURRENT APPLICATION NUMBER: US/09/416,901B
/ CURRENT FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 63
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-09-416-901B-63

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VNLDAEF 9

RESULT 74
US-09-416-901B-64
/ Sequence 64, Application US/09416901B
/ Patent No. 6699671
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
/ FILE REFERENCE: 29915/6280A
/ CURRENT APPLICATION NUMBER: US/09/416,901B
/ CURRENT FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 64
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-09-416-901B-64

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VKMDAEF 9

RESULT 75
US-09-548-376D-63
/ Sequence 63, Application US/09548376D
/ Patent No. 6706485
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
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/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
/ TITLE OF INVENTION: AND USES
/ FILE REFERENCE: 29915/6280F
/ CURRENT APPLICATION NUMBER: US/09/548,376D
/ CURRENT FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 63
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized peptide
US-09-548-376D-63

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VNLDAEF 9

RESULT 76
US-09-548-376D-64
/ Sequence 64, Application US/09548376D
/ Patent No. 6706485
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
/ TITLE OF INVENTION: AND USES
/ FILE REFERENCE: 29915/6280F
/ CURRENT APPLICATION NUMBER: US/09/548,376D
/ CURRENT FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 64
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized peptide
US-09-548-376D-64

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 3 VKMDAEF 9

RESULT 77
```

US-09-794-927A-63
; Sequence 63, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-927A-63

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 78
US-09-794-927A-64
; Sequence 64, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-927A-64

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 79
US-09-548-373D-63
; Sequence 63, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280B
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-373D-63

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 80
US-09-548-373D-64
; Sequence 64, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280B
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-373D-64

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred.No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VKMDAEF 9

RESULT 81

US-09-724-961-3
; Sequence 3, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-3

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred.No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 4 VKMDAEF 10

RESULT 82

US-09-724-961-4
; Sequence 4, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-4

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred.No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VKMDAEF 9

RESULT 83

US-09-724-961-5
; Sequence 5, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-5

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred.No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 2 VKMDAEF 8

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RESULT 84
US-09-724-961-6
; Sequence 6, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from A11792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-6

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 1 VKMDAEF 7

RESULT 85
US-09-795-847B-63
; Sequence 63, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-795-847B-63

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 1 VKMDAEF 7

RESULT 86
US-09-795-847B-64
; Sequence 64, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-795-847B-64

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 3 VKMDAEF 9

RESULT 87
US-09-580-018-3
; Sequence 3, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-795-847B-63
```

```
Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXXAEF 7
Db 3 VKMDAEF 9
```

```
RESULT 86
US-09-795-847B-64
; Sequence 64, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-795-847B-64
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Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXXAEF 7
Db 3 VKMDAEF 9
```

```
RESULT 87
US-09-580-018-3
; Sequence 3, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
```

```
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-3

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VKMDAEF 10

RESULT 88
US-09-580-018-4
; Sequence 4, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-4

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 89
US-09-580-018-5
; Sequence 5, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
```

```
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-5

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 90
US-09-580-018-6
; Sequence 6, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-6

Query Match          100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 1 VKMDAEF 7

RESULT 91
US-09-724-551-3
; Sequence 3, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
```


; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-09-724-551-3

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 10;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

Db 4 VKMDAEF 10

RESULT 92

US-09-724-551-4

; Sequence 4, Application US/09724551

; Patent No. 6787637

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/09/724,551

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-09-724-551-4

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 10;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

Db 3 VKMDAEF 9

RESULT 93

US-09-724-551-5

; Sequence 5, Application US/09724551

; Patent No. 6787637

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/09/724,551

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-09-724-551-5

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 10;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

Db 2 VKMDAEF 8

RESULT 94

US-09-724-551-6

; Sequence 6, Application US/09724551

; Patent No. 6787637

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/09/724,551

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-09-724-551-6

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 10;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

Db 1 VKMDAEF 7

RESULT 95

US-09-869-414-63

; Sequence 63, Application US/09869414

; Patent No. 6790610

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

```
; FILE REFERENCE: 29915/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-869-414-63
```

```
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXXAEF 7
Db 3 VNLDADF 9
```

RESULT 96

```
US-09-869-414-64
; Sequence 64, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-869-414-64
```

```
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VKMDADF 9
```

RESULT 97

```
US-09-548-366F-63
; Sequence 63, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; OTHER INFORMATION: THEREOF
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```
; FILE REFERENCE: 29915/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366F-63
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```
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXXAEF 7
Db 3 VNLDADF 9
```

RESULT 98

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US-09-548-366F-64
; Sequence 64, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366F-64
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```
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXXAEF 7
Db 3 VKMDADF 9
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RESULT 99

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US-09-548-368D-63
; Sequence 63, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
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QY      1 VXXAEEF 7
Db      3 VMDAEF 9

RESULT 103
PCT-US91-07290-1
; Sequence 1, Application PC/TUS9107290
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07290
; FILING DATE: 19911004
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
; REFERENCE/DOCKET NUMBER: 17796-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Xaa5
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
PCT-US91-07290-1
Query Match 100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEEF 7
Db      3 VMDAEF 9

RESULT 104
PCT-US94-07043A-3
; Sequence 3, Application PC/TUS9407043A

```

```

; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10889
; FILING DATE: November 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/880,914
; FILING DATE: May 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pamela A. Simonton
; REGISTRATION NUMBER: 31,060
; REFERENCE/DOCKET NUMBER: MTI 224.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-3
Query Match 100.0%; Score 7; DB 5; Length 11;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEEF 7
Db      4 VNLDAAEF 10

RESULT 105
PCT-US94-07043A-7
; Sequence 7, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600

```

OPERATING SYSTEM: MS-DOS
CURRENT APPLICATION DATA:
SOFTWARE: WordPerfect 5.1
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-7

Query Match 100.0%; Score 7; DB 5; Length 11;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 4 VKMDAEF 10

RESULT 106
US-07-737-431A-1
Sequence 1. Application US/07737431A
Patent No. 5378607
GENERAL INFORMATION:
APPLICANT: Chelladurai, Mohanathasan
APPLICANT: Honn, Kenneth V.
APPLICANT: Walz, Daniel A.
TITLE OF INVENTION: Method For Testing For
TITLE OF INVENTION: The Presence of Metastatic
TITLE OF INVENTION: Tumor Cells
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,431A
FILING DATE: 19910729
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: RORDC 4.1-3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5378607e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE:
DESCRIPTION: Polypeptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HLA DR and Human Ovarian Carcinoma
STRAIN: N/A
INDIVIDUAL ISOLATE: N/A
CELL TYPE: Human
FEATURE:
NAME/KEY: Partial polypeptide of HLA-DR
LOCATION: N/A
IDENTIFICATION METHOD: Sequencing
OTHER INFORMATION: Polypeptide
US-07-737-431A-1
Query Match 100.0%; Score 7; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 74;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 6 VIIQAEF 12

RESULT 107
PCT-US94-07043A-2
Sequence 2. Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-2
```

```
Query Match 100.0%; Score 7; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 74;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
|::|||
Db 4 VKMDAEF 10
```

```
RESULT 108
US-09-724-566A-72
; Sequence 72, Application US/09724566A
; Patent No. 6627739
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P10-P4' staD-V peptide inhibitor
```

```
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 10
; OTHER INFORMATION: Xaa is statine moiety
US-09-724-566A-72
Query Match 100.0%; Score 7; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
|:|:|
Db 8 VNXVAEF 14
```

```
RESULT 109
US-09-724-566A-97
; Sequence 97, Application US/09724566A
; Patent No. 6627739
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP-derived fragment P10-P4' (D-V)
US-09-724-566A-97
```

```
Query Match 100.0%; Score 7; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
|::|||
Db 8 VNLVAEF 14
```

```
RESULT 110
US-09-471-669A-72
; Sequence 72, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-0064300S
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 14
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P10-P4'staD-V
; OTHER INFORMATION: peptide inhibitor
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa is statine moiety
US-09-471-669A-72

Query Match          100.0%; Score 7; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      8 VNXVAEF 14

RESULT 111
US-09-471-669A-97
; Sequence 97, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: APP-derived
; OTHER INFORMATION: fragment P10-P4' (D-V)
US-09-471-669A-97

Query Match          100.0%; Score 7; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      8 VNLVAEF 14

RESULT 112
US-09-548-372D-71
; Sequence 71, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
```

```
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-548-372D-71

Query Match          100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      5 VKMDAEF 11

RESULT 113
US-09-548-367D-71
; Sequence 71, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-548-367D-71

Query Match          100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      5 VKMDAEF 11

RESULT 114
US-09-551-853D-71
; Sequence 71, Application US/09551853D
```

```
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
; US-09-551-853D-71

Query Match      100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
       |:::|||
Db      5 VKMDAEF 11

RESULT 115
US-09-416-901B-71
; Sequence 71, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280A
; CURRENT APPLICATION NUMBER: US/09/416,901B
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-09-416-901B-71

Query Match      100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
       |:::|||
Db      5 VKMDAEF 11
```

```
RESULT 116
US-09-548-376D-71
; Sequence 71, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
; US-09-548-376D-71

Query Match      100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
       |:::|||
Db      5 VKMDAEF 11
```

```
RESULT 117
US-09-794-927A-71
; Sequence 71, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
; US-09-794-927A-71

Query Match      100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```



```
QY 1 VXXAAEF 7
   |:::|
Db 5 VKMDAEF 11

RESULT 118
US-09-548-373D-71
; Sequence 71, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-548-373D-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 5 VKMDAEF 11

RESULT 119
US-09-795-847B-71
; Sequence 71, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 15
```

```
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-795-847B-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 5 VKMDAEF 11

RESULT 120
US-09-869-414-71
; Sequence 71, Application US/09869414
; Patent No. 6790610
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-869-414-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 5 VKMDAEF 11

RESULT 121
US-09-548-366F-71
; Sequence 71, Application US/09548366F
; Patent No. 6797487
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
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; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366F-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXDAEF 7
|::|||
Db 5 VKMDAEF 11

RESULT 122

US-09-548-368D-71
; Sequence 71, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/548,368D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-368D-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXDAEF 7
|::|||
Db 5 VKMDAEF 11

RESULT 123

US-09-794-925A-71
; Sequence 71, Application US/09794925A
; Patent No. 6828117
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-794-925A-71

Query Match 100.0%; Score 7; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXDAEF 7
|::|||
Db 5 VKMDAEF 11

RESULT 124

PCT-US94-07043A-1
; Sequence 1, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,

; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10889
; FILING DATE: November 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/880,914
; FILING DATE: May 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pamela A. Simonton
; REGISTRATION NUMBER: 31,060
; REFERENCE/DOCKET NUMBER: MTI 224.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2340
; TELEFAX: (203) 937-2795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-07043A-1

Query Match 100.0%; Score 7; DB 5; Length 16;
Best Local Similarity 57.1%; Pred. No. 98;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 4 VKMDAEF 10

RESULT 125

US-08-149-975A-3
; Sequence 3, Application US/08149975A
; Patent No. 5849600
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; APPLICANT: Honda, Toshiyuki
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-149-975A-3

Query Match 100.0%; Score 7; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 1 VKMDAEF 7

RESULT 126

US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobsen-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Healin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-18

Query Match 100.0%; Score 7; DB 2; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 127

US-08-802-981-112
; Sequence 112, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
;
; US-08-802-981-112
;
; Query Match 100.0%; Score 7; DB 3; Length 21;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VXXADEF 7
; DB 8 VNLDAEF 14
;
; RESULT 128
; US-08-802-981-113
; Sequence 113, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
;
; FEATURE:
; NAME/KEY: Modified-site
;
; US-08-802-981-114
;
; Query Match 100.0%; Score 7; DB 3; Length 21;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VXXADEF 7
; DB 8 VKLDAEF 14
;
; RESULT 129
; US-08-802-981-114
; Sequence 114, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
;
; FEATURE:
; NAME/KEY: Modified-site
```

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;
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
; US-08-802-981-114

Query Match      100.0%; Score 7; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 8 VKMDAEF 14

RESULT 130
US-08-660-531-18
; Sequence 18, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-531-18

Query Match      100.0%; Score 7; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 131
US-09-634-955B-24
; Sequence 24, Application US/09634955B
; Patent No. 6511834
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Cook, William James
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-134
; CURRENT APPLICATION NUMBER: US/09/634,955B
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/192,002
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 24
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3-beta hydroxysteroid dehydrogenase domain
; US-09-634-955B-24

Query Match      100.0%; Score 7; DB 4; Length 23;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VTGGAEF 10

RESULT 132
US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

US-08-141-324-11

Query Match 100.0%; Score 7; DB 1; Length 27;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 6 VKMDAEF 12

RESULT 133

US-08-141-324-12

; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-141-324-12

Query Match 100.0%; Score 7; DB 1; Length 27;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 6 VLDLAEF 12

RESULT 134

US-08-541-902-11

; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James

; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-541-902-11

Query Match 100.0%; Score 7; DB 1; Length 27;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 6 VKMDAEF 12

RESULT 135

US-08-541-902-12

; Sequence 12, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-541-902-12

Query Match 100.0%; Score 7; DB 1; Length 27;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 6 VLDLDAEF 12

RESULT 136
US-08-659-984A-17
; Sequence 17, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-659-984A-17

Query Match 100.0%; Score 7; DB 2; Length 30;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 24 VNLDAEF 30

RESULT 137
US-08-660-531-17
; Sequence 17, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-660-531-17

Query Match 100.0%; Score 7; DB 3; Length 30;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 1 VXXAAEF 7
```

```
Db      24 VNLDAEF 30
;
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligopeptide substrate
US-09-471-669A-53
Query Match      100.0%; Score 7; DB 4; Length 30;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VYXXAEF 7
DB      24 VNLDAEF 30
;
;
RESULT 140
US-08-659-984A-16
; Sequence 16, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: peptide
;
US-08-659-984A-16
Query Match      100.0%; Score 7; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db      24 VNLDAEF 30
;
;
RESULT 139
US-09-471-669A-53
; Sequence 53, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-53
Query Match      100.0%; Score 7; DB 4; Length 30;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VYXXAEF 7
DB      24 VNLDAEF 30
;
;
RESULT 138
US-09-724-566A-53
; Sequence 53, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-53
Query Match      100.0%; Score 7; DB 4; Length 30;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VYXXAEF 7
DB      24 VNLDAEF 30
;
;
RESULT 137
US-09-471-669A-53
; Sequence 53, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
```


Qy 1 VXXAAEF 7
|:::|
Db 15 VNLDAEP 21

RESULT 141
US-08-660-531-16
; Sequence 16, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-16

Query Match 100.0%; Score 7; DB 3; Length 33;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 15 VNLDAEP 21

RESULT 142
US-09-724-566A-63
; Sequence 63, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P26-P4'sw peptide substrate
US-09-724-566A-63

Query Match 100.0%; Score 7; DB 4; Length 33;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 27 VNLDAEF 33

RESULT 143
US-09-471-669A-63
; Sequence 63, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P26-P4'sw peptide substrate
US-09-471-669A-63

Query Match 100.0%; Score 7; DB 4; Length 33;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7
|:::|
Db 27 VNLDAEF 33

RESULT 144
US-08-659-984A-15
; Sequence 15, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-15

Query Match 100.0%; Score 7; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7
|:::|
Db 24 VNLDAEF 30

RESULT 145
US-08-660-531-15
; Sequence 15, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-15

Query Match 100.0%; Score 7; DB 3; Length 42;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7
|:::|
Db 24 VNLDAEF 30

RESULT 146
US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobson, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 7; DB 1; Length 45;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 7 VKMDAEF 13

RESULT 147
US-08-123-659A-5
Sequence 5, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: US/08/123,659A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 7; DB 1; Length 45;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 7 VKMDAEF 13

RESULT 148
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US/08/464,247A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 7; DB 1; Length 45;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 7 VKMDAEF 13

RESULT 149
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 7; DB 1; Length 45;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 7 VKMDAEF 13

RESULT 150
US-08-415-751-12
; Sequence 12, Application US/08415751
; Patent No. 5643772
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND
; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS AND KIT
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILLIPS, MOORE, LEMPJO & FINLEY
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,751
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/071,880
; FILING DATE: June 1, 1993
; APPLICATION NUMBER: 07/891,301
; FILING DATE: May 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Dolezalova
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (415) 324-1677
; TELEFAX: (415) 324-1678
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; NAME/KEY: Positions coded by nonsense codons are
; NAME/KEY: identified as xaa.
US-08-415-751-12

Query Match 100.0%; Score 7; DB 1; Length 47;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 7 VELAAEF 13

RESULT 151
US-09-560-883-1
; Sequence 1, Application US/09560883
; Patent No. 6638711
; GENERAL INFORMATION:
; APPLICANT: Bush, Ashley
; APPLICANT: Huang, Xudong
; APPLICANT: Atwood, Craig
; APPLICANT: Tanzi, Rudolph
; TITLE OF INVENTION: Method of Screening for Drugs Useful in Treating Alzheimer's D
; FILE REFERENCE: 0609 481001/REF/KKV
; CURRENT APPLICATION NUMBER: US/09/560,883
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/380,704
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04683
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 08/816,122
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Human amyloid protein precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (4)..(45)
; OTHER INFORMATION: A beta
US-09-560-883-1

Query Match 100.0%; Score 7; DB 4; Length 48;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 1 VKMDAEF 7

RESULT 152
US-09-173-887-5
; Sequence 5, Application US/09173887
; Patent No. 6245884
; GENERAL INFORMATION:
; APPLICANT: Hook, Vivian Y.H.
; TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE: P-AS 3337

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; CURRENT APPLICATION NUMBER: US/09/173,887
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0.
; SEQ ID NO 5
; LENGTH: 53
; TYPE: PRT
; ORGANISM: mammalian
US-09-173-887-5

Query Match 100.0%; Score 7; DB 3; Length 53;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 1 VKMDAEF 7

RESULT 153
US-09-797-543-5
; Sequence 5, Application US/09797543
; Patent No. 6627409
; GENERAL INFORMATION:
; APPLICANT: Hook, Vivian Y.H.
; TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE: P-AS 4579
; CURRENT APPLICATION NUMBER: US/09/797,543
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/173,887
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 53
; TYPE: PRT
; ORGANISM: 'Axial Seamount' polynoid polychaete
US-09-797-543-5

Query Match 100.0%; Score 7; DB 4; Length 53;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 1 VKMDAEF 7

RESULT 154
US-09-288-143-158
; Sequence 158, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 158
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-288-143-158

Query Match 100.0%; Score 7; DB 4; Length 56;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 36 VAARAEF 42

RESULT 155
US-08-371-930-25
; Sequence 25, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-371-930-25

Query Match 100.0%; Score 7; DB 1; Length 58;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEEF 7
|:::|
Db 44 VKMDAEF 50

RESULT 156

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PCT-US94-01712-25
; Sequence 25, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US94-01712-25

Query Match 100.0%; Score 7; DB 5; Length 58;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
Db 44 VKMDAEF 50

RESULT 157
US-08-484-969-3
; Sequence 3, Application US/08484969
; Patent No. 5679531
; GENERAL INFORMATION:
; APPLICANT: Konig, Gerhard
; APPLICANT: Graham, Paul
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
; TITLE OF INVENTION: Peptide
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegratti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

PCT-US94-01712-25
; APPLICATION NUMBER: US/08/484,969
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 95,216
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 4.5
; OTHER INFORMATION: /label= Beta
; OTHER INFORMATION: /note= "Beta cleavage site in App"
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 20..21
; OTHER INFORMATION: /label= Alpha
; OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17"
; OTHER INFORMATION: of BA4."
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 46..47
; OTHER INFORMATION: /label= Gamma
; OTHER INFORMATION: /note= "Gamma cleavage site in APP"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 5..47
; OTHER INFORMATION: /label= BA4
; OTHER INFORMATION: /note= "BA4 peptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 33..56
; OTHER INFORMATION: /label= Tm
; OTHER INFORMATION: /note= "Transmembrane region of APP"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..32
; OTHER INFORMATION: /label= Ex
; OTHER INFORMATION: /note= "N-terminal extracellular part of App"
; US-08-484-969-3

Query Match 100.0%; Score 7; DB 1; Length 59;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
Db 2 VKMDAEF 8

RESULT 158
US-08-472-627-3
; Sequence 3, Application US/08472627
; Patent No. 5693753
; GENERAL INFORMATION:
; APPLICANT: Konig, Gerhard
; APPLICANT: Graham, Paul
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
; TITLE OF INVENTION: Peptide
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegratti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago

```

```
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,627
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17"
OTHER INFORMATION: /note= "of BA4."
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
OTHER INFORMATION: /note= "Transmembrane region of App"
FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-472-627-3
Query Match 100.0%; Score 7; DB 1; Length 59;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXAEF 7
DB 2 VKMDAEF 8
RESULT 159
US-08-388-463-3
Sequence 3, Application US/08388463
Patent No. 5786180
GENERAL INFORMATION:
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APPLICANT: Konig, Gerhard
APPLICANT: Graham, Paul
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
TITLE OF INVENTION: Peptide
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegetti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,463
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17"
OTHER INFORMATION: /note= "of BA4."
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
OTHER INFORMATION: /note= "Transmembrane region of App"
FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-388-463-3
Query Match 100.0%; Score 7; DB 1; Length 59;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXAEF 7
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Db      |:::|
      2 VKMDAEF 8

RESULT 160
US-09-621-976-6908
; Sequence 6908, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6908
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6908

Query Match      100.0%; Score 7; DB 4; Length 61;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
      |:::|
Db      48 VQPSAEF 54

RESULT 161
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-4

Query Match      100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
      |:::|
Db      7 VKMDAEF 13

RESULT 162
US-08-462-859A-4
; Sequence 4, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-4

Query Match      100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAEF 7
      |:::|
Db      7 VKMDAEF 13

RESULT 163
US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
```



```
;
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-123-659A-3

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 7 VKMDAEF 13

RESULT 164
US-08-123-659A-4
; Sequence 4, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-123-659A-4

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 7 VKMDAEF 13

RESULT 165
US-08-464-247A-3
; Sequence 3, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-4117
; TELEFAX: 201-683-2158
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-247A-3

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 7 VKMDAEF 13

RESULT 166
```

```
US-08-464-247A-4
; Sequence 4, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-4

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7
Db 7 VKMDAEF 13

RESULT 167
US-08-464-248A-3
; Sequence 3, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-4
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US-08-464-248A-3
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-3

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7
Db 7 VKMDAEF 13

RESULT 168
US-08-464-248A-4
; Sequence 4, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-4
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Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 7 VKMDAEF 13

RESULT 169
US-09-248-796A-24127
; Sequence 24127, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24127
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24127

Query Match 100.0%; Score 7; DB 4; Length 66;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 54 VKIAAEF 60

RESULT 170
US-09-243-675-4
; Sequence 4, Application US/09243675
; Patent No. 6291442
; GENERAL INFORMATION:
; APPLICANT: Gary I. Yellen
; TITLE OF INVENTION: Pharmacological Modulators of
; FILE REFERENCE: 0838.1023-001
; CURRENT APPLICATION NUMBER: US/09/243,675
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/073,482
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Potassium Ion channel
; PUBLICATION INFORMATION:
; AUTHORS: Liu Y., et al.
; JOURNAL: Neuron
; VOLUME: 1997
; PAGES: 175-184
; DATE: 1997-07-01
US-09-243-675-4

Query Match 100.0%; Score 7; DB 3; Length 67;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 51 VNNFAEF 57

RESULT 171
US-09-027-258-1
; Sequence 1, Application US/09027258
; Patent No. 6670182
; GENERAL INFORMATION:
; APPLICANT: Pruss, Rebecca
; APPLICANT: Huggins, John
; APPLICANT: Rautmann, Guy
; APPLICANT: Cordell, Barbara
; APPLICANT: Scardina, Jan
; APPLICANT: Mischak, Ron
; TITLE OF INVENTION: IMPROVED ASSAYS FOR BETA-AMYLOID
; TITLE OF INVENTION: PROCESSING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marsh, David R
; REGISTRATION NUMBER: P-41,182
; REFERENCE/DOCKET NUMBER: 03561.0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6904
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6670182e
US-09-027-258-1

Query Match 100.0%; Score 7; DB 4; Length 67;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 23 VKMDAEF 29

RESULT 172
US-09-543-681A-7973
; Sequence 7973, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7973
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7973

Query Match 100.0%; Score 7; DB 4; Length 68;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 28 VNAQAEF 34

RESULT 173

517197-52
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 52:
; LENGTH: 68
5177197-52

Query Match 100.0%; Score 7; DB 6; Length 68;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 48 VLGTAEF 54

RESULT 174

5177197-52
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 52:
; LENGTH: 68
5177197-52

Query Match 100.0%; Score 7; DB 6; Length 68;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 48 VLGTAEF 54

RESULT 175

US-09-270-767-61614
; Sequence 61614, Application US/09270767

; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61614
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61614

Query Match 100.0%; Score 7; DB 4; Length 70;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 21 VQKLAEF 27

RESULT 176

US-09-248-796A-16636
; Sequence 16636, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16636
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16636

Query Match 100.0%; Score 7; DB 4; Length 74;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 35 VMKAAEF 41

RESULT 177

US-08-225-757B-7
; Sequence 7, Application US/08225757B
; Patent No. 5506133
; GENERAL INFORMATION:
; APPLICANT: YU, ET AL.
; TITLE OF INVENTION: Superoxide Dismutase-4
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSER: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/225,757B
; APPLICATION NUMBER: US/08/225,757B
; FILING DATE: 11 APR-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-225-757B-7

Query Match 100.0%; Score 7; DB 1; Length 78;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 18 VHVHAEF 24

RESULT 178
US-09-949-016-9298
; Sequence 9298, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 9298
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9298

Query Match 100.0%; Score 7; DB 4; Length 89;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 82 VSNAAEF 88

RESULT 179
US-09-134-000C-6592
; Sequence 6592, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6592
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-6592

Query Match 100.0%; Score 7; DB 4; Length 91;
Best Local Similarity 57.1%; Pred. No. 5.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 47 VNFPAEF 53

RESULT 180
US-09-621-976-4330
; Sequence 4330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4330
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-621-976-4330

Query Match 100.0%; Score 7; DB 4; Length 94;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 81 VENMAEF 87

RESULT 181
US-08-311-731A-79
; Sequence 79, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 411
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
```

;
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
; US-08-311-731A-79

Query Match 100.0%; Score 7; DB 4; Length 95;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 36 VRDAEF 42

RESULT 182
US-08-479-078-27
; Sequence 27, Application US/08479078
; Patent No. 5814466
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: Method for Assaying for a Substance that
; TITLE OF INVENTION: Affects an SH2-Phosphorylated Ligand Regulatory System
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street, West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,078
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda M. Kurdzyk
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids

;
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-479-078-27

Query Match 100.0%; Score 7; DB 2; Length 96;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 29 VKDAEF 35

RESULT 183
US-09-640-211A-830
; Sequence 830, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Sherk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 830
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-09-640-211A-830

Query Match 100.0%; Score 7; DB 4; Length 96;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 38 VKTAEF 44

RESULT 184
US-09-270-767-43511
; Sequence 43511, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7328-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43511
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-43511

Query Match 100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 32 VDPAAEF 38

```
RESULT 185
US-08-404-831-2
; Sequence 2, Application US/08404831
; Patent No. 5817626
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis, Howard Benjamin, Marc B. Garnick,
; APPLICANT: Malcolm L. Gelfer, Arvind Hundal, Laura Kasman,
; APPLICANT: Gary Musso, Ethan R. Signer, and James Wakefield
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggrega
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,831
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A. (EAH)
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: PPI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-404-831-2

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 2 VKMDAEF 8

RESULT 186
US-08-612-785B-2
; Sequence 2, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-2

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEEF 7
Db 2 VKMDAEF 8

RESULT 187
US-08-475-579A-2
; Sequence 2, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggrega
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-475-579A-2

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 188
US-08-920-162A-2
; Sequence 2, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findels, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PFI-016CP4
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-920-162A-2
```

```
Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 189
US-08-339-708A-10
; Sequence 10, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-708A-10

Query Match 100.0%; Score 7; DB 3; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 190
US-08-339-708A-12
; Sequence 12, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
```



```

; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-708A-12

```

```

Query Match      100.0%; Score 7; DB 3; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VXXXAEF 7
Db      2 VNLDAEF 8

```

```

RESULT 191
US-09-356-931-2
; Sequence 2, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-356-931-2

```

```

Query Match      100.0%; Score 7; DB 3; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VXXXAEF 7
Db      2 VKMDAEF 8

```

```

RESULT 192
US-08-703-675C-2
; Sequence 2, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995

```

```
; PRIOR APPLICATION DATA: USN 08/616,081
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-703-675C-2

Query Match 100.0%; Score 7; DB 3; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 2 VKMDAEF 8

RESULT 193
US-08-617-267C-2
; Sequence 2, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-2

Query Match 100.0%; Score 7; DB 3; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 2 VKMDAEF 8

RESULT 194
US-09-519-019A-2
; Sequence 2, Application US/09519019A
; Patent No. 6610658
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A.
; APPLICANT: Phillips, Kathryn
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; TITLE OF INVENTION: MODULATORS OF A-AMYLOID PEPTIDE
; TITLE OF INVENTION: AGGREGATION
; FILE REFERENCE: PPI-068CP
; CURRENT APPLICATION NUMBER: US/09/519,019A
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/122,736
; PRIOR FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide
US-09-519-019A-2

Query Match 100.0%; Score 7; DB 4; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 2 VKMDAEF 8

RESULT 195
US-09-895-443A-2
; Sequence 2, Application US/09895443A
; Patent No. 6689752
; GENERAL INFORMATION:
; APPLICANT: FINDERIS, MARK A.
; APPLICANT: GEFTER, MALCOLM L.
; APPLICANT: MUSSO, GARY
; APPLICANT: SIGNER, ETHAN R.
; APPLICANT: WAKEFIELD, JAMES
; APPLICANT: MOLINAUX, SUSAN
; APPLICANT: CHIN, JOSEPH
; APPLICANT: LEE, JUNG-JA
; APPLICANT: KELLEY, MICHAEL
; APPLICANT: KOMAR-PANICUCCI, SONJA
; APPLICANT: ARICO-MUENDEL, CHRISTOPHER C.
; APPLICANT: PHILLIPS, KATHRYN
; APPLICANT: HAYWARD, NEIL J.
; TITLE OF INVENTION: MODULATORS OF BETA-AMYLOID PEPTIDE
; TITLE OF INVENTION: AGGREGATION COMPRISING D-AMINO ACIDS
; FILE REFERENCE: PPI-0016CF4CN2
; CURRENT APPLICATION NUMBER: US/09/895,443A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/356931
; PRIOR FILING DATE: 1990-07-19
; PRIOR APPLICATION NUMBER: 08/920162
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;; PRIOR FILING DATE: 1997-08-27
;; PRIOR APPLICATION NUMBER: 08/548998
;; PRIOR FILING DATE: 1995-10-27
;; PRIOR APPLICATION NUMBER: 08/616081
;; PRIOR FILING DATE: 1996-03-14
;; PRIOR APPLICATION NUMBER: 08/703675
;; PRIOR FILING DATE: 1996-08-27
;; PRIOR APPLICATION NUMBER: 08/897342
;; PRIOR FILING DATE: 1997-07-21
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 103
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-895-443A-2

Query Match 100.0%; Score 7; DB 4; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 196

US-10-395-290-2
;; Sequence 2, Application US/10395290
;; Patent No. 6831066
;; GENERAL INFORMATION:
;; APPLICANT: Findeis, Mark A.
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Olson, Gary L.
;; APPLICANT: Self, Christopher
;; TITLE OF INVENTION: MODULATORS OF A-AMYLOID PEPTIDE
;; FILE REFERENCE: PPI-068CP
;; CURRENT APPLICATION NUMBER: US/10/395,290
;; CURRENT FILING DATE: 2003-03-24
;; PRIOR APPLICATION NUMBER: US/09/519,019A
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/122,736
;; PRIOR FILING DATE: 1999-03-04
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 103
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Polypeptide
US-10-395-290-2

Query Match 100.0%; Score 7; DB 4; Length 103;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 197

US-08-729-345-1
;; Sequence 1, Application US/08729345
;; Patent No. 5849999
;; GENERAL INFORMATION:
;; APPLICANT: Neve, Rachael L.
;; APPLICANT: Berger-Sweeney, Joanne
;; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL
;; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
;; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,345
;; FILING DATE: 16-OCT-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04843/027001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 105 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-729-345-1

Query Match 100.0%; Score 7; DB 2; Length 105;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
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Db 4 VKMDAEF 10

RESULT 198

US-09-471-276-1338
;; Sequence 1338, Application US/09471276
;; Patent No. 6822072
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Duclert A.
;; APPLICANT: Giordano, J.Y.
;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;; Patent No. 6822072
;; FILE REFERENCE: GENSET 025CP1
;; CURRENT APPLICATION NUMBER: US/09/471,276
;; CURRENT FILING DATE: 1999-12-21
;; EARLIER APPLICATION NUMBER: 09/057,719
;; EARLIER FILING DATE: 1998-04-09
;; EARLIER APPLICATION NUMBER: 09/069,047
;; EARLIER FILING DATE: 1998-04-28
;; EARLIER APPLICATION NUMBER: PCT/IB99/00712
;; EARLIER FILING DATE: 1999-04-09
;; NUMBER OF SEQ ID NOS: 1622
;; SOFTWARE: Patent.pm
;; SEQ ID NO 1338
;; LENGTH: 110
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -84...-1

US-09-471-276-1338

Query Match 100.0%; Score 7; DB 4; Length 110;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 64 VPXIAEF 70

RESULT 199

US-08-311-731A-185
; Sequence 185, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-185

Query Match 100.0%; Score 7; DB 4; Length 112;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 53 VRDAEF 59

RESULT 200

US-09-640-211A-1105
; Sequence 1105, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-1105

Query Match 100.0%; Score 7; DB 4; Length 115;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 55 VWRPAEF 61

Search completed: November 15, 2005, 11:00:34
Job time : 31.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:55:49 ; Search time 117 Seconds
(without alignments)
25.033 Million cell updates/sec

Title: SEQ59

Perfect score: 7

Sequence: 1 vxxaef 7

Scoring table: OLIGO0X

Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 7

Total number of hits satisfying chosen parameters: 3208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US16_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	7	100.0	7	9	US-09-796-264-27
2	7	100.0	7	9	US-09-845-226-27
3	7	100.0	7	9	US-09-795-903A-27
4	7	100.0	7	13	US-10-057-505-10
5	7	100.0	7	14	US-10-293-580-44
6	7	100.0	7	16	US-10-820-953-27
7	7	100.0	7	16	US-10-773-754-27
8	7	100.0	7	18	US-10-957-433-14
9	7	100.0	7	18	US-10-625-854-207
10	7	100.0	7	20	US-11-089-918-78
11	7	100.0	7	20	US-11-090-866-78

12	7	100.0	7	20	US-11-069-377-78	Sequence 78, Appl
13	7	100.0	7	20	US-11-090-872-78	Sequence 78, Appl
14	7	100.0	7	20	US-11-090-399-78	Sequence 78, Appl
15	7	100.0	8	9	US-09-794-927-67	Sequence 67, Appl
16	7	100.0	8	9	US-09-795-847-67	Sequence 67, Appl
17	7	100.0	8	9	US-09-794-743-67	Sequence 67, Appl
18	7	100.0	8	9	US-09-794-748-67	Sequence 67, Appl
19	7	100.0	8	9	US-09-796-264-28	Sequence 28, Appl
20	7	100.0	8	9	US-09-794-925-67	Sequence 67, Appl
21	7	100.0	8	9	US-09-681-442-67	Sequence 67, Appl
22	7	100.0	8	9	US-09-845-226-28	Sequence 28, Appl
23	7	100.0	8	9	US-09-795-903A-28	Sequence 28, Appl
24	7	100.0	8	10	US-09-869-414-67	Sequence 67, Appl
25	7	100.0	8	14	US-10-032-818-5	Sequence 5, Appl
26	7	100.0	8	15	US-10-427-208-52	Sequence 52, Appl
27	7	100.0	8	15	US-10-652-927-67	Sequence 67, Appl
28	7	100.0	8	15	US-10-652-830-67	Sequence 67, Appl
29	7	100.0	8	16	US-10-281-092-15	Sequence 15, Appl
30	7	100.0	8	16	US-10-281-092-51	Sequence 51, Appl
31	7	100.0	8	16	US-10-652-045-67	Sequence 67, Appl
32	7	100.0	8	16	US-10-820-953-28	Sequence 28, Appl
33	7	100.0	8	16	US-10-773-754-28	Sequence 28, Appl
34	7	100.0	8	16	US-10-773-754-35	Sequence 35, Appl
35	7	100.0	8	16	US-10-476-935-67	Sequence 67, Appl
36	7	100.0	8	17	US-10-480-954-257	Sequence 257, App
37	7	100.0	8	17	US-10-480-954-258	Sequence 258, App
38	7	100.0	8	17	US-10-480-954-259	Sequence 259, App
39	7	100.0	8	17	US-10-480-954-260	Sequence 260, App
40	7	100.0	8	17	US-10-480-954-263	Sequence 263, App
41	7	100.0	8	17	US-10-480-954-264	Sequence 264, App
42	7	100.0	8	17	US-10-477-076-67	Sequence 67, Appl
43	7	100.0	8	18	US-10-625-854-208	Sequence 208, Appl
44	7	100.0	8	18	US-10-625-854-219	Sequence 219, App
45	7	100.0	8	18	US-10-817-979-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-09-796-264-27
; Sequence 27, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-796-264-27

Query Match 100.0%; Score 7; DB 9; Length 7;

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-845-226-27

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 1 VNLAEEF 7

RESULT 2
US-09-845-226-27
; Sequence 27, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-845-226-27

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
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Db 1 VNLAEEF 7

RESULT 3
US-09-795-903A-27
; Sequence 27, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-795-903A-27

Query Match      100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 1 VNLAEEF 7

RESULT 4
US-10-057-505-10
; Sequence 10, Application US/10057505
; Publication No. US20020164674A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: AURORA BIOSCIENCES CORPORATION
; APPLICANT: TS'EN, Roger
; APPLICANT: HEIM, Roger
; APPLICANT: CUBITT, Andrew
; TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
; FILE REFERENCE: REGEN1260-3
; CURRENT APPLICATION NUMBER: US/10/057,505
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 08/792,553
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: US 09/396,003
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker moiety
US-10-057-505-10

Query Match      100.0%; Score 7; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 1 VKMDAEF 7

RESULT 5
US-10-293-580-44
; Sequence 44, Application US/10293580
; Publication No. US20030170767A1
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; APPLICANT: Cubitt, Andrew B.
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AURO1270 (08366/031001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: b-Secretase for amyloid precursor protein
US-10-293-580-44

Query Match 100.0%; Score 7; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 1 VKMDAEF 7

RESULT 6
US-10-820-953-27
; Sequence 27, Application US/10820953
; Publication No. US20040167075A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J. N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/10/820,953
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-10-820-953-27

Query Match 100.0%; Score 7; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 1 VNLAAEF 7

RESULT 7
US-10-773-754-27
; Sequence 27, Application US/10773754
; Publication No. US20040220079A1
; GENERAL INFORMATION:
; APPLICANT: Koelsch, Gerald
; APPLICANT: Tang, Jordan J. N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 022266-000930US
; CURRENT APPLICATION NUMBER: US/10/773,754
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US 60/141,363

; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/210,292
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 09/845,226
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: memapsin 2 inhibitor substrate analogue OM99-1
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)-(4)
; OTHER INFORMATION: Xaa at positions 3 and 4 represent Leu and Ala
; OTHER INFORMATION: with the peptide bond substituted by a
; OTHER INFORMATION: transition-state isostere hydroxyethylene
; OTHER INFORMATION: (-CH(OH)-CH-2-) group
US-10-773-754-27

Query Match 100.0%; Score 7; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 1 VNXAAEF 7

RESULT 8
US-10-957-433-14
; Sequence 14, Application US/10957433
; Publication No. US20050153310A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Frank
; APPLICANT: Lewis, Martin Ken
; APPLICANT: Shultz, John W.
; APPLICANT: Wood, Keith V.
; APPLICANT: Butler, Braeden
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Luciferase Biosensor
; FILE REFERENCE: 341.027US1
; CURRENT APPLICATION NUMBER: US/10/957,433
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/510,187
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic -secretase site for amyloid precursor protein
US-10-957-433-14

Query Match 100.0%; Score 7; DB 18; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|

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Db      1 VKMDAEF 7

RESULT 9
US-10-625-854-207
; Sequence 207, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362 0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 207
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-207

Query Match      100.0%; Score 7; DB 18; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
       |:|:|
Db      1 VKMDAEF 7

RESULT 10
US-11-089-918-78
; Sequence 78, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

Query Match      100.0%; Score 7; DB 18; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
       |:|:|
Db      1 VKMDAEF 7

RESULT 11
US-11-090-866-78
; Sequence 78, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

Query Match      100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
       |:|:|
Db      1 VMXVAEF 7

RESULT 12
US-11-069-377-78

Query Match      100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
       |:|:|
Db      1 VMXVAEF 7
```



```

; Sequence 78, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-069-377-78

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. NO. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 1 VMXVAEF 7

RESULT 13
US-11-090-872-78
; Sequence 78, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28

```

```

; Sequence 78, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-872-78

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. NO. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 1 VMXVAEF 7

RESULT 14
US-11-090-399-78
; Sequence 78, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3

```

; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-399-78

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 1 VMXAAEF 7

RESULT 15

US-09-794-927-67
; Sequence 67, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Van, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-67

Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 2 VKMDAEF 8

RESULT 16

US-09-795-847-67
; Sequence 67, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Van, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-67

Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 2 VKMDAEF 8

RESULT 17

US-09-794-743-67
; Sequence 67, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Van, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-67

Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 2 VKMDAEF 8

```
RESULT 18
US-09-794-748-67
; Sequence 67, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-67

Query Match      100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 19
US-09-796-264-28
; Sequence 28, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-67

Query Match      100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 20
US-09-794-925-67
; Sequence 67, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-925-67

Query Match      100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 21
US-09-681-442-67
; Sequence 67, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-796-264-28

Query Match      100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 20
US-09-794-925-67
; Sequence 67, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-925-67

Query Match      100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VKMDAEF 8

RESULT 21
US-09-681-442-67
; Sequence 67, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
```

```
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-681-442-67
```

```
Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8
```

```
RESULT 22
US-09-845-226-28
; Sequence 28, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT FILING DATE: 2001-04-30
; CURRENT APPLICATION NUMBER: US/09/845,226
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-845-226-28
```

```
Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
|:::|
Db 2 VNLAAEF 8
```

```
RESULT 23
US-09-795-903A-28
```

```
; Sequence 28, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-795-903A-28
```

```
Query Match 100.0%; Score 7; DB 9; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
|:::|
Db 2 VNLAAEF 8
```

```
RESULT 24
US-09-869-414-67
; Sequence 67, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-869-414-67
```

```
Query Match 100.0%; Score 7; DB 10; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
```

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 25

US-10-032-818-5
; Sequence 5, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Koelsch, Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 2932.1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-032-818-5

Query Match 100.0%; Score 7; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 2 VNLAEF 8

RESULT 26

US-10-427-208-52
; Sequence 52, Application US/10427208
; Publication No. US20030200555A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hazuda, Daria J.
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Lai, Ming-Tain
; APPLICANT: Xu, Min
; APPLICANT: Shi, Xiao-Ping
; APPLICANT: Simon, Adam J.
; APPLICANT: Wu, Guoxin
; APPLICANT: Li, Yueming
; APPLICANT: Register, Robert B.
; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED
; FILE REFERENCE: 21052
; CURRENT APPLICATION NUMBER: US/10/427,208
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-427-208-52

Query Match 100.0%; Score 7; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 27

US-10-652-927-67
; Sequence 67, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, App. Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280N3
; CURRENT APPLICATION NUMBER: US/10/652,927
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-927-67

Query Match 100.0%; Score 7; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 28

US-10-652-830-67
; Sequence 67, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-830-67

Query Match 100.0%; Score 7; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
Db 2 VKNDAEF 8

RESULT 29
US-10-281-092-15
; Sequence 15, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Arun K.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Bilcer, Geoffrey
; APPLICANT: Chang, Wanpin
; APPLICANT: Hong, Lin
; APPLICANT: Koelsch, Gerald E.
; APPLICANT: Loy, Jeffrey A.
; APPLICANT: Turner, Robert T., III
; APPLICANT: Devasumadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; FILE REFERENCE: 2932.1001-004
; CURRENT APPLICATION NUMBER: US/10/281,092
; CURRENT FILING DATE: 2002-10-23
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 10/032,818
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: PCT US01/50826
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/335,952
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/333,545
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/348,464
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/348,615
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/390,804
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/397,557
; PRIOR FILING DATE: 2002-07-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: memapsin 2 substrate
US-10-281-092-15

Query Match 100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|

Db 2 VNLADEF 8

RESULT 30
US-10-281-092-51
; Sequence 51, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Arun K.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Bilcer, Geoffrey
; APPLICANT: Chang, Wanpin
; APPLICANT: Hong, Lin
; APPLICANT: Koelsch, Gerald E.
; APPLICANT: Loy, Jeffrey A.
; APPLICANT: Turner, Robert T., III
; APPLICANT: Devasumadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; FILE REFERENCE: 2932.1001-004
; CURRENT APPLICATION NUMBER: US/10/281,092
; CURRENT FILING DATE: 2002-10-23
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 10/032,818
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: PCT US01/50826
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/335,952
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/333,545
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/348,464
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/348,615
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/390,804
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/397,557
; PRIOR FILING DATE: 2002-07-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial peptide
US-10-281-092-51

Query Match 100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
Db 2 VNLADEF 8

RESULT 31
US-10-652-045-67
; Sequence 67, Application US/10652045
; Publication No. US20040166507A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280N2
; CURRENT APPLICATION NUMBER: US/10/652,045
; CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: 09/794,925
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 67
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-652-045-67

Query Match 100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VKMDAEF 8

RESULT 32
US-10-820-953-28
Sequence 28, Application US/10820953
Publication No. US20040167075A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J. N.
APPLICANT: Ghosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: OMRF 182
CURRENT APPLICATION NUMBER: US/10/820,953
PRIOR FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US/09/603,713
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/141,363
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-10-820-953-28

Query Match 100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VNLAAEF 8

RESULT 33
US-10-773-754-28
Sequence 28, Application US/10773754
Publication No. US20040220079A1
GENERAL INFORMATION:
APPLICANT: Koelsch, Gerald
APPLICANT: Tang, Jordan J. N.
APPLICANT: Hong, Lin
APPLICANT: Ghosh, Arun K.
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 022266-000930US
CURRENT APPLICATION NUMBER: US/10/773,754
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: US 60/141,363
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/210,292
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US 09/603,713
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 09/845,226
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: octapeptide
OTHER INFORMATION: upon which synthetic memapsin 2 inhibitor
OTHER INFORMATION: substrate analogue OM99-2 is based
US-10-773-754-28

Query Match 100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 2 VNLAAEF 8

RESULT 34
US-10-773-754-35
Sequence 35, Application US/10773754
Publication No. US20040220079A1
GENERAL INFORMATION:
APPLICANT: Koelsch, Gerald
APPLICANT: Tang, Jordan J. N.
APPLICANT: Hong, Lin
APPLICANT: Ghosh, Arun K.
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 022266-000930US
CURRENT APPLICATION NUMBER: US/10/773,754
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: US 60/141,363
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 60/178,368

```

; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/210,292
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 09/845,226
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 35
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: memapsin 2 inhibitor substrate analogue OM99-2
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(5)
; OTHER INFORMATION: Xaa at positions 4 and 5 represent Leu and Ala
; OTHER INFORMATION: with the peptide bond substituted by a
; OTHER INFORMATION: transition-state isostere hydroxyethylene
; OTHER INFORMATION: (-CH(OH)-CH-2-) group
US-10-773-754-35

Query Match      100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VNXXAEF 8

RESULT 35
US-10-476-935-67
; Sequence 67, Application US/10476935
; Publication No. US20040234976A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280M1
; CURRENT APPLICATION NUMBER: US/10/476,935
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-10-476-935-67

Query Match      100.0%; Score 7; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VKWDAEF 8

RESULT 36
US-10-480-954-257
; Sequence 257, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-257

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 2 VNLDAEF 8

RESULT 37
US-10-480-954-258
; Sequence 258, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 8
; TYPE: PRT
```



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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-258

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 38
US-10-480-954-259
; Sequence 259, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-259

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 39
US-10-480-954-260
; Sequence 260, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 20886YP

```

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; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-260

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNLAAEF 8

RESULT 40
US-10-480-954-263
; Sequence 263, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(8)
; OTHER INFORMATION: Xaa = Cyclohexylglycine
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-263

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 2 VNXAAEF 8

```

```
RESULT 41
US-10-480-954-264
; Sequence 264, Application US/10480954
; Publication No. US20050032190A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Stephen F.
; APPLICANT: Bruce, James E.
; APPLICANT: Chen-Dodson, Elizabeth
; APPLICANT: Garsky, Victor
; APPLICANT: Li, Yueming
; APPLICANT: Sardana, Mohinder
; APPLICANT: Shafer, Jules A.
; APPLICANT: Tang, Xiaoting
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; FILE REFERENCE: 20886YP
; CURRENT APPLICATION NUMBER: US/10/480,954
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/15590
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(8)
; OTHER INFORMATION: Xaa = Cyclohexylalanine
; OTHER INFORMATION: Beta-Secretase Cleavage Site
US-10-480-954-264

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      2 VNXAAEF 8
|::|||

RESULT 42
US-10-477-076-67
; Sequence 67, Application US/10477076
; Publication No. US20050080232A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280M2
; CURRENT APPLICATION NUMBER: US/10/477,076
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8

QY      1 VXXAAEF 7
Db      2 VNXAAEF 8
|::|||

RESULT 43
US-10-625-854-208
; Sequence 208, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-208

Query Match      100.0%; Score 7; DB 18; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      2 VKMDAEF 8
|::|||

RESULT 44
US-10-625-854-219
; Sequence 219, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-219

Query Match      100.0%; Score 7; DB 18; Length 8;
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-10-477-076-67

Query Match      100.0%; Score 7; DB 17; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      2 VKMDAEF 8
|::|||

RESULT 43
US-10-625-854-208
; Sequence 208, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-208

Query Match      100.0%; Score 7; DB 18; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      2 VKMDAEF 8
|::|||

RESULT 44
US-10-625-854-219
; Sequence 219, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-219

Query Match      100.0%; Score 7; DB 18; Length 8;
```

```
; Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 1 VKMDAEF 7

RESULT 45
US-10-817-979-70
; Sequence 70, Application US/10817979
; Publication No. US20050196398A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/40065
; CURRENT APPLICATION NUMBER: US/10/817,979
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 09/668,314
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-817-979-70

Query Match 100.0%; Score 7; DB 18; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 2 VKMDAEF 8

RESULT 46
US-10-817-979-71
; Sequence 71, Application US/10817979
; Publication No. US20050196398A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/40065
; CURRENT APPLICATION NUMBER: US/10/817,979
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 09/668,314
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-817-979-71

Query Match 100.0%; Score 7; DB 18; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 2 VNLDAEF 8

RESULT 47
US-11-089-918-81
; Sequence 81, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-089-918-81

Query Match 100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
```

```

Db      2 VMXVAEF 8
|:|:|
RESULT 48
US-11-090-866-81
; Sequence 81, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-866-81
Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
|:|:|
Db      2 VMXVAEF 8
|:|:|
RESULT 50
US-11-090-872-81
; Sequence 81, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-866-81
Query Match      100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
|:|:|
Db      2 VMXVAEF 8
|:|:|
RESULT 49
US-11-069-377-81
; Sequence 81, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Prigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-872-81

```

```

Query Match          100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:|:|
DB      2 VMXAAEF 8

```

```

RESULT 51
US-11-090-399-81
; Sequence 81, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Erigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-11-090-399-81

```

```

Query Match          100.0%; Score 7; DB 20; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:|:|
DB      2 VMXAAEF 8

```

RESULT 52

```

US-09-896-874-8
; Sequence 8, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-8

```

```

Query Match          100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:|:|
DB      3 VNLDAEF 9

```

```

RESULT 53
US-09-816-876-4
; Sequence 4, Application US/09816876
; Publication No. US20020019403A1
; GENERAL INFORMATION:
; APPLICANT: Hom, Roy
; APPLICANT: Mamo, Shumeye
; APPLICANT: Tung, Jay
; APPLICANT: Gailunas, Andrea
; APPLICANT: Varghese, John
; APPLICANT: Fang, Larry
; TITLE OF INVENTION: Methods to Treat Alzheimer's Disease
; FILE REFERENCE: 01-1736-D
; CURRENT APPLICATION NUMBER: US/09/816,876
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,528
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-816-876-4

```

```

Query Match          100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:|:|
DB      3 VNLDAEF 9

```

```

RESULT 54
US-09-896-139-8
; Sequence 8, Application US/09896139
; Patent No. US2002012825A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.

```

```
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,139
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-8

Query Match          100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9

RESULT 55
US-09-895-843-8
; Sequence 8, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
```

```
US-09-895-843-8

Query Match          100.0%; Score 7; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAAEF 9

RESULT 56
US-09-908-943A-113
; Sequence 113, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Van, Rigiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Peptide sequence
US-09-908-943A-113
```

```
Query Match          100.0%; Score 7; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 2 VNLDAAEF 8
```

```
RESULT 57
US-09-895-871-8
; Sequence 8, Application US/09895871
; Publication No. US20030096864A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Hom, Roy
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.21USU1
; CURRENT APPLICATION NUMBER: US/09/895,871
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-871-8
```

Query Match 100.0%; Score 7; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 58

US-09-874-350A-209
; Sequence 209, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is D form of tetrahydroisoquinoline-3-carboxylic acid
US-09-874-350A-209

Query Match 100.0%; Score 7; DB 11; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 59

US-10-016-717-6
; Sequence 6, Application US/10016717
; Publication No. US20020132281A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Vivian Y.H.
; TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE: P-AS 5031
; CURRENT APPLICATION NUMBER: US/10/016,717
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 09/173,887
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 09/294,987
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mammalian
US-10-016-717-6

Query Match 100.0%; Score 7; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VKMDAEF 9

RESULT 60

US-10-192-625-8
; Sequence 8, Application US/10192625
; Publication No. US20030083353A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chruscziel, Robert A.
; TITLE OF INVENTION: Diaminediols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1645-B
; CURRENT APPLICATION NUMBER: US/10/192,625
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,305
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/334,480
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-625-8

Query Match 100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 61

US-10-192-424-8
; Sequence 8, Application US/10192424
; Publication No. US20030083356A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chruscziel, Robert A.
; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-154-A
; CURRENT APPLICATION NUMBER: US/10/192,424
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/204,128
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/327,424
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
US-10-192-424-8

```
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-424-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 3 VNLDAAEF 9

RESULT 62
US-10-183-126A-8
; Sequence 8, Application US/10183126A
; Publication No. US20030083518A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia and Upjohn Company
; APPLICANT: John, Varghese
; APPLICANT: Hom, Roy
; APPLICANT: Tucker, John
; TITLE OF INVENTION: Substituted Alcohols Useful in Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1704-C
; CURRENT APPLICATION NUMBER: US/10/183,126A
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptides substrate with cleavage site of beta-sec
; OTHER INFORMATION: etase and with optionally detectable tag.
US-10-183-126A-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 3 VNLDAAEF 9

RESULT 63
US-10-171-343-8
; Sequence 8, Application US/10171343
; Publication No. US20030092747A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Rober A.
; TITLE OF INVENTION: Aminedols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 01-1644-B
; CURRENT APPLICATION NUMBER: US/10/171,343
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/297,827
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/333,084
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-171-343-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 3 VNLDAAEF 9

RESULT 64
US-10-264-707-8
; Sequence 8, Application US/10264707
; Publication No. US20030125365A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-264-707-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |::|||
Db 3 VNLDAAEF 9

RESULT 65
US-10-066-319-3
; Sequence 3, Application US/10066319
; Publication No. US20030147810A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Brian D.
; APPLICANT: Rehemtulla, Alnawaz
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REPORTING
; TITLE OF INVENTION: OF PROTEASE ACTIVITY WITHIN THE SECRETORY PATHWAY
; FILE REFERENCE: 11203-007001
; CURRENT APPLICATION NUMBER: US/10/066,319
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-066-319-3

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```



```
QY      1 VXXXAEF 7
|::|||
Db      3 VKWDAEF 9

RESULT 66
US-10-066-319-4
; Sequence 4, Application US/10066319
; Publication No. US20030147810A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Brian D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REPORTING
; FILE REFERENCE: 11203-007001
; CURRENT APPLICATION NUMBER: US/10/066,319
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-319-4

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
|::|||
Db      3 VNLDAEF 9

RESULT 67
US-10-337-075-8
; Sequence 8, Application US/10337075
; Publication No. US20030166580A1
; GENERAL INFORMATION:
; APPLICANT: Warpehoski, Martha A.
; TITLE OF INVENTION: Substituted Amino Carboxamides for the Treatment of Alzheimer's D
; FILE REFERENCE: 01-1795-C
; CURRENT APPLICATION NUMBER: US/10/337,075
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/345,316
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/350,419
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal biotin
US-10-337-075-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
|::|||
Db      3 VNLDAEF 9

RESULT 68
US-10-160-777-8
; Sequence 8, Application US/10160777
; Publication No. US20030166717A1
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varghese, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal biotin
US-10-160-777-8

Query Match      100.0%; Score 7; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
|::|||
Db      3 VNLDAEF 9

RESULT 69
US-10-192-543-8
; Sequence 8, Application US/10192543
; Publication No. US20040019086A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Aminoalcohols for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-156-A
; CURRENT APPLICATION NUMBER: US/10/192,543
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,129
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal biotin
US-10-192-543-8

Query Match      100.0%; Score 7; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
```

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 70

US-10-299-739-8
; Sequence 8, Application US/10299739
; Publication No. US20040039064A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Romero, Arthur G.
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Christina, McGrain M.
; TITLE OF INVENTION: Amine 1,2- and 1,3-Diol Compounds
; FILE REFERENCE: 01-1724-B
; CURRENT APPLICATION NUMBER: US/10/299,739
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: 60/333,081
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/334,000
; PRIOR FILING DATE: 2001-11-18
; PRIOR APPLICATION NUMBER: 60/362,752
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-299-739-8

Query Match 100.0%; Score 7; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 71

US-10-685-898-107
; Sequence 107, Application US/10685898
; Publication No. US20040121412A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: BETA SECRETASE EXOSITE BINDING PEPTIDES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING BETA SECRETASE MODULATORS
; FILE REFERENCE: D0252 NP
; CURRENT APPLICATION NUMBER: US/10/685,898
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,679
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthesized Peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1).(1)
; OTHER INFORMATION: wherein amino acid may be modified with a
; OTHER INFORMATION: 7-methoxycoumarin-4-acetyl group
; FEATURE:

; NAME/KEY: MOD RES
; LOCATION: (9).(9)
; OTHER INFORMATION: Wherein amino acid 9 may be modified with a carboxylated
; OTHER INFORMATION: dinitrophenyl group
US-10-685-898-107

Query Match 100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:|:|:|
Db 2 VNLDAEF 8

RESULT 72

US-10-658-959A-8
; Sequence 8, Application US/10658959A
; Publication No. US20040180939A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Varghese, John
; APPLICANT: Maillard, Michel
; APPLICANT: Beck, James
; APPLICANT: Balgwin, Eric
; APPLICANT: Hughes, Robert
; APPLICANT: Pulley, Shon
; APPLICANT: TenBrink, Ruth
; TITLE OF INVENTION: Acetyl 2-Hydroxy-1,3-Diaminoalkanes
; FILE REFERENCE: 02-793-C
; CURRENT APPLICATION NUMBER: US/10/658,959A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,453
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/452,231
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/491,757
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-658-959A-8

Query Match 100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:|:|:|
Db 3 VNLDAEF 9

RESULT 73

US-10-801-487-113
; Sequence 113, Application US/10801487
; Publication No. US20040241792A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281F
; CURRENT APPLICATION NUMBER: US/10/801,487
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-487-113

Query Match      100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VNLDADF 8

RESULT 74
US-10-801-938-113
; Sequence 113, Application US/10801938
; Publication No. US20040253706A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; CURRENT APPLICATION NUMBER: US/10/801,938
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-938-113

Query Match      100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VNLDADF 8

RESULT 75
US-10-801-509-113
; Sequence 113, Application US/10801509
; Publication No. US20040254341A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281C
; CURRENT APPLICATION NUMBER: US/10/801,509
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-509-113

Query Match      100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VNLDADF 8

RESULT 76
US-10-801-486-113
; Sequence 113, Application US/10801486
; Publication No. US20040254342A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281B
; CURRENT APPLICATION NUMBER: US/10/801,486
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-486-113

Query Match      100.0%; Score 7; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 2 VNLDADF 8

RESULT 77
US-10-621-311-1
; Sequence 1, Application US/10621311
; Publication No. US20050014160A1
; GENERAL INFORMATION:
; APPLICANT: Kumaraswamy, Sriam
; APPLICANT: Achyuthan, Komandoor
; APPLICANT: Shi, Xiaobo
; APPLICANT: Bergstedt, Troy
; APPLICANT: Rinninsland, Duncan
; APPLICANT: McBranch, Frauke
; APPLICANT: Whitten, David
; TITLE OF INVENTION: Assays for Protease Enzyme Activity
; FILE REFERENCE: 8971-032-27
; CURRENT APPLICATION NUMBER: US/10/621,311
; CURRENT FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: segment capable of recognizing and interacting
; OTHER INFORMATION: with beta-secretase
US-10-621-311-1
```

US-10-621-311-1

Query Match 100.0%; Score 7; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VNLDADF 9

RESULT 78

US-10-828-582-8
; Sequence 8, Application US/10828582
; Publication No. US20050054690A1
; GENERAL INFORMATION:
; APPLICANT: Aquino, Jose
; APPLICANT: John, Varghese
; APPLICANT: Tucker, John
; APPLICANT: Hom, Roy
; APPLICANT: Pulley, Shon
; APPLICANT: Tenbrink, Ruth
; TITLE OF INVENTION: Phenacyl 2-hydroxy-3-diaminoalkanes
; FILE REFERENCE: 03-169-A
; CURRENT APPLICATION NUMBER: US/10/828,582
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: 60/464,676
; PRIOR FILING DATE: 2003-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-828-582-8

Query Match 100.0%; Score 7; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VNLDADF 9

RESULT 79

US-10-801-493-113
; Sequence 113, Application US/10801493
; Publication No. US20050096457A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281E
; CURRENT APPLICATION NUMBER: US/10/801,493
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-493-113

Query Match 100.0%; Score 7; DB 17; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 2 VNLDADF 8

RESULT 80

US-10-625-854-209
; Sequence 209, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039--)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-209

Query Match 100.0%; Score 7; DB 18; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VKMDADF 9

RESULT 81

US-10-625-854-220
; Sequence 220, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039--)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-220

Query Match 100.0%; Score 7; DB 18; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 2 VKMDADF 8

RESULT 82
US-10-625-854-230
; Sequence 230, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; TITLE OF INVENTION: beta-amyloid formation and/or aggregation
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625.854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-625-854-230

Query Match 100.0%; Score 7; DB 18; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
|:::|
Db 1 VKMDAEF 7

RESULT 83
US-11-075-161-8
; Sequence 8, Application US/11075161
; Publication No. US20050159459A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-154-D2
; CURRENT APPLICATION NUMBER: US/11/075,161
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/204,128
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/327,424
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 10/192,424
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-11-075-161-8

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 84
US-11-076-161-8
; Sequence 8, Application US/11076161

; Publication No. US20050165069A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 02-154-D1
; CURRENT APPLICATION NUMBER: US/11/076,161
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/204,128
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/327,424
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 10/192,424
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-11-076-161-8

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 85
US-11-089-918-52
; Sequence 52, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
; US-11-089-918-52

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |::|||
 Db 3 VNLDAAEF 9

RESULT 86

US-11-089-918-73
 ; Sequence 73, Application US/11089918
 ; Publication No. US20050164327A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Gurigbal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; FILE REFERENCE: 228-US-NEW2C9
 ; CURRENT FILING DATE: 2005-03-25
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: US 09/471,669
 ; PRIOR FILING DATE: 1999-12-24
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 73
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: P4-P4'staD-V peptide inhibitor
 ; NAME/KEY: MOD_RES
 ; LOCATION: 5
 ; OTHER INFORMATION: Xaa is statine moiety
 US-11-089-918-73

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |::|||
 Db 3 VNXXAAEF 9

RESULT 87

US-11-089-918-82
 ; Sequence 82, Application US/11089918
 ; Publication No. US20050164327A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Gurigbal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand

; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; FILE REFERENCE: 228-US-NEW2C9
 ; CURRENT FILING DATE: 2005-03-25
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: US 09/471,669
 ; PRIOR FILING DATE: 1999-12-24
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 82
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: APP fragment P5-P4' wt
 US-11-089-918-82

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |::|||
 Db 3 VNMDAAEF 9

RESULT 88

US-11-089-918-83
 ; Sequence 83, Application US/11089918
 ; Publication No. US20050164327A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Gurigbal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; FILE REFERENCE: 228-US-NEW2C9
 ; CURRENT FILING DATE: 2005-03-25
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: US 09/471,669
 ; PRIOR FILING DATE: 1999-12-24
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
US-11-089-918-83
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
|:::|
DB 3 VNLDAAEF 9
```

RESULT 89

```
US-11-089-918-84
; Sequence 84, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-84
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
|:::|
DB 3 VKLDAEF 9
```

RESULT 90

```
US-11-089-918-85
; Sequence 85, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-85
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEEF 7
|:::|
DB 3 VKFDAEF 9
```

RESULT 91

```
US-11-089-918-86
; Sequence 86, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
```

```

; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-86

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |::|||
Db       3 VNFADEF 9

```

RESULT 92

```

US-11-089-918-87
; Sequence 87, Application US/11089918
; Publication No. US20050164327A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-87

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |::|||
Db       3 VKMAAEF 9

```

RESULT 93

```

US-11-089-918-88
; Sequence 88, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-88

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |::|||
Db       3 VNLADEF 9

```

RESULT 94

```

US-11-089-918-89
; Sequence 89, Application US/11089918
; Publication No. US20050164327A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708

```



```

; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-89

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VXXAAEF 7
        |:::|
Db      3 VKLAEEF 9

```

```

RESULT 95
US-11-089-918-90
; Sequence 90, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-90

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VXXAAEF 7
        |:::|

```

```

Db      3 VKMLAEF 9

```

```

RESULT 96
US-11-089-918-91
; Sequence 91, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-91

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VXXAAEF 7
        |:::|
Db      3 VMLAEF 9

```

```

RESULT 97
US-11-089-918-92
; Sequence 92, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918

```

```
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-92
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred.No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 3 VKLAAEF 9
```

```
RESULT 98
US-11-089-918-93
; Sequence 93, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-93
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred.No. 1.7e+06;
```

```
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXAAEF 7
Db 3 VKFAAEF 9
```

```
RESULT 99
US-11-089-918-94
; Sequence 94, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-94
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred.No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 3 VNFAAEF 9
```

```
RESULT 100
US-11-089-918-95
; Sequence 95, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
```

```
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-089-918-95
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
|:::|
DB 3 VKFLAEF 9
```

RESULT 101

```
US-11-089-918-96
; Sequence 96, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guricbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089,918
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
```

US-11-089-918-96

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
|:::|
DB 3 VNFLAEF 9
```

RESULT 102

```
US-11-090-866-52
; Sequence 52, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guricbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-11-090-866-52
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
|:::|
DB 3 VNFLAEF 9
```

RESULT 103

```
US-11-090-866-73
; Sequence 73, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guricbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
```

```
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P4-P4'staD-V peptide inhibitor
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Xaa is statine moiety
US-11-090-866-73
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:|:|
DB       3 VNXVAEF 9
```

```
RESULT 104
US-11-090-866-82
; Sequence 82, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
```

```
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-11-090-866-82
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:|:|
DB       3 VKMDAEF 9
```

```
RESULT 105
US-11-090-866-83
; Sequence 83, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
US-11-090-866-83
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:|:|
DB       3 VNLDAEF 9
```

```
RESULT 106
US-11-090-866-84
; Sequence 84, Application US/11090866
; Publication No. US20050164294A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-866-84

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXAAEF 7
Db      3 VKLDAEF 9

; RESULT 107
; US-11-090-866-85
; Sequence 85, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-866-84

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXAAEF 7
Db      3 VKLDAEF 9
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-866-86

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXAAEF 7
Db      3 VKFDAEF 9

; RESULT 108
; US-11-090-866-86
; Sequence 86, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-866-86

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VXXAAEF 7
Db      3 VNFDAEF 9
```

RESULT 109

US-11-090-866-87
; Sequence 87, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-87

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VVMAAEF 9

RESULT 110

US-11-090-866-88
; Sequence 88, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-88

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VVMAAEF 9

RESULT 111

US-11-090-866-89
; Sequence 89, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-89

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

Db 3 VKLAAEF 9
|:::|

RESULT 112

```
US-11-090-866-90
; Sequence 90, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-90
```

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|

Db 3 VKMLAEF 9

RESULT 113

```
US-11-090-866-91
; Sequence 91, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
```

Query Match 100.0%; Score 7; DB 20; Length 9;

```
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-91
```

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|

Db 3 VNLLAEF 9

RESULT 114

```
US-11-090-866-92
; Sequence 92, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-92
```

Query Match 100.0%; Score 7; DB 20; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0;

QY 1 VXXAAEF 7
|:|:|
Db 3 VKLAAEF 9

RESULT 115

US-11-090-866-93
; Sequence 93, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-93

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|
Db 3 VKFAAEF 9

RESULT 116

US-11-090-866-94
; Sequence 94, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-866-94

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|
Db 3 VNFAAEF 9

RESULT 117

US-11-090-866-95
; Sequence 95, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090,866
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: APP fragment
US-11-090-866-95

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VKFLAEF 9

RESULT 118

US-11-090-866-96
; Sequence 96, Application US/11090866
; Publication No. US20050164294A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, Normand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; FILE REFERENCE: 228-US-NEW2C12

; CURRENT APPLICATION NUMBER: US/11/090,866

; CURRENT FILING DATE: 2005-03-25

; PRIOR FILING DATE: 2000-11-28

; PRIOR FILING DATE: 2000-11-28

; PRIOR FILING DATE: 2000-02-10

; PRIOR FILING DATE: 1999-12-24

; PRIOR FILING DATE: 1999-02-10

; PRIOR FILING DATE: 1999-02-10

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 96

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: APP fragment

US-11-090-866-96

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VNFLEAF 9

RESULT 119

US-11-069-377-52

; Sequence 52, Application US/11069377

; Publication No. US20050170489A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, Normand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-11-069-377-52

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VNLDAEF 9

RESULT 120

US-11-069-377-73

; Sequence 73, Application US/11069377

; Publication No. US20050170489A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, Normand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; FILE REFERENCE: 228-US-NEW2C8

; CURRENT APPLICATION NUMBER: US/11/069,377

; CURRENT FILING DATE: 2005-02-28

; PRIOR FILING DATE: 2000-11-28

; PRIOR FILING DATE: 2000-11-28

; PRIOR FILING DATE: 2000-02-10

; PRIOR FILING DATE: 1999-02-10

; PRIOR FILING DATE: 1999-02-10

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 73

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

```
; OTHER INFORMATION: P4-P4'stad-V peptide inhibitor
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Xaa is statine moiety
US-11-069-377-73
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |::|||
Db       3 VNXVAEF 9
```

RESULT 121

```
US-11-069-377-82
; Sequence 82, Application US/11069377
; Publication No. US20050170489A1
```

GENERAL INFORMATION:

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-11-069-377-82
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |::|||
Db       3 VKMDAEF 9
```

RESULT 122

```
US-11-069-377-83
; Sequence 83, Application US/11069377
; Publication No. US20050170489A1
```

GENERAL INFORMATION:

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
```

```
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
US-11-069-377-83
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |::|||
Db       3 VNLDAEF 9
```

RESULT 123

```
US-11-069-377-84
; Sequence 84, Application US/11069377
; Publication No. US20050170489A1
```

GENERAL INFORMATION:

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-84

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VKLDAEF 9

RESULT 124

US-11-069-377-85
; Sequence 85, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377

; CURRENT FILING DATE: 2005-02-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment

US-11-069-377-85

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VKLDAEF 9

RESULT 125

US-11-069-377-86
; Sequence 86, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377

; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment

US-11-069-377-86

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAEF 7
|:::|
Db 3 VNPDAEF 9

RESULT 126

US-11-069-377-87
; Sequence 87, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377

; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

US-11-069-377-87

```

; OTHER INFORMATION: APP fragment
US-11-069-377-87

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLAAEF 9

RESULT 127
US-11-069-377-88
; Sequence 88, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-89

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLAAEF 9

RESULT 128
US-11-069-377-89
; Sequence 89, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-90

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLAAEF 9

RESULT 129
US-11-069-377-90
; Sequence 90, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-90

```

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 DB 3 VKMLAEP 9

RESULT 130

US-11-069-377-91

; Sequence 91, Application US/11069377
 ; Publication No. US20050170489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Guribhal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: 228-US-NEW2C8
 ; CURRENT APPLICATION NUMBER: US/11/069,377
 ; CURRENT FILING DATE: 2005-02-28
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 91
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: APP fragment
 ; US-11-069-377-91

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 DB 3 VNLAAEP 9

RESULT 131

US-11-069-377-92

; Sequence 92, Application US/11069377
 ; Publication No. US20050170489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Guribhal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: 228-US-NEW2C8
 ; CURRENT APPLICATION NUMBER: US/11/069,377
 ; CURRENT FILING DATE: 2005-02-28
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 92
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: APP fragment
 ; US-11-069-377-92

Query Match 100.0%; Score 7; DB 20; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 DB 3 VKLLAEP 9

RESULT 132

US-11-069-377-93

; Sequence 93, Application US/11069377
 ; Publication No. US20050170489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Guribhal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, Normand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: 228-US-NEW2C8
 ; CURRENT APPLICATION NUMBER: US/11/069,377
 ; CURRENT FILING DATE: 2005-02-28
 ; PRIOR APPLICATION NUMBER: US 09/723,722
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 93
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: APP fragment
 ; US-11-069-377-93

Query Match 100.0%; Score 7; DB 20; Length 9;

```

Best Local Similarity 57.1%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0;

QY 1 VXXAAEF 7
Db 3 VKFAAEF 9

RESULT 133
US-11-069-377-94
; Sequence 94, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-94

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKFLAEF 9

RESULT 135
US-11-069-377-96
; Sequence 96, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-96

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNFAAEF 9

RESULT 134
US-11-069-377-95
; Sequence 95, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-95

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNFAAEF 9

RESULT 134
US-11-069-377-95
; Sequence 95, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-069-377-95

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VXXAAEF 7
Db      3 VNFLEAF 9

RESULT 136
US-11-090-872-52
; Sequence 52, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-11-090-872-52
Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VNFLEAF 9

RESULT 137
US-11-090-872-73
; Sequence 73, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

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; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P4-P4'stad-V peptide inhibitor
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Xaa is statine moiety
US-11-090-872-73
Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VNXVAEF 9

RESULT 138
US-11-090-872-82
; Sequence 82, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-11-090-872-82

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 139
US-11-090-872-83
; Sequence 83, Application US/11090872
; Publication No. US2005017788A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-84

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKLDAEF 9

RESULT 141
US-11-090-872-85
; Sequence 85, Application US/11090872
; Publication No. US2005017788A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-11-090-872-83

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 140
US-11-090-872-84
; Sequence 84, Application US/11090872
; Publication No. US2005017788A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand

```



```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-85
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:::|
DB      3 VKFDAEF 9
```

RESULT 142

```
US-11-090-872-86
; Sequence 86, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
```

```
US-11-090-872-86
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:::|
DB      3 VNFDAEF 9
```

RESULT 143

```
US-11-090-872-87
; Sequence 87, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-87
```

```
Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VXXAAEF 7
        |:::|
DB      3 VKMAAEF 9
```

RESULT 144

```
US-11-090-872-88
; Sequence 88, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
```

```

; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-88

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VNLAAEF 9

```

RESULT 145

```

US-11-090-872-89
; Sequence 89, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-89

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VKLAAEF 9

```

RESULT 146

```

US-11-090-872-90
; Sequence 90, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-90

```

```

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
        |:::|
Db       3 VKMLAEF 9

```

RESULT 147

```

US-11-090-872-91
; Sequence 91, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708

```

```

; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-91

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
       |:::|
Db      3 VLLAAEF 9

```

```

RESULT 148
US-11-090-872-92
; Sequence 92, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-92

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
       |:::|

```

```

Db      3 VKLLAEF 9

```

```

RESULT 149
US-11-090-872-93
; Sequence 93, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-93

```

```

Query Match      100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VXXAAEF 7
       |:::|
Db      3 VKFAAEF 9

```

```

RESULT 150
US-11-090-872-94
; Sequence 94, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872

```

```
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-94
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAEEF 7
|::|||
Db 3 VNFPAEF 9
```

```
RESULT 151
US-11-090-872-95
; Sequence 95, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-95
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
```

```
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXAEEF 7
|::|||
Db 3 VNFPAEF 9
```

```
RESULT 152
US-11-090-872-96
; Sequence 96, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-872-96
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAEEF 7
|::|||
Db 3 VNFPAEF 9
```

```
RESULT 153
US-11-090-399-52
; Sequence 52, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
```

```
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-11-090-399-52
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VNLDAEF 9
```

RESULT 154

```
US-11-090-399-73
; Sequence 73, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P4-P4'staad-v peptide inhibitor
```

```
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Xaa is statine moiety
US-11-090-399-73
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VNXVAEF 9
```

RESULT 155

```
US-11-090-399-82
; Sequence 82, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4' wt
US-11-090-399-82
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXXAEF 7
Db 3 VKMDAEF 9
```

RESULT 156

```
US-11-090-399-83
; Sequence 83, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
```

```
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
US-11-090-399-83
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
```

```
RESULT 157
US-11-090-399-84
; Sequence 84, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
```

```
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-84
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
```

```
RESULT 158
US-11-090-399-85
; Sequence 85, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-85
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXAAEF 7
Db 3 VKLDAEF 9
```

```
RESULT 159
US-11-090-399-86
; Sequence 86, Application US/11090399
; Publication No. US20050196839A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-399-86
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VNPDAAEF 9
```

```
RESULT 160
US-11-090-399-87
; Sequence 87, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
```

```
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-399-87
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VNMAAEF 9
```

```
RESULT 161
US-11-090-399-88
; Sequence 88, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
; US-11-090-399-88
```

```
Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VXXXAEF 7
Db 3 VNMAAEF 9
```

```
RESULT 162
US-11-090-399-89
; Sequence 89, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-89

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VKLAEEF 9

RESULT 163
US-11-090-399-90
; Sequence 90, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-90

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VKLAEEF 9

RESULT 164
US-11-090-399-91
; Sequence 91, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-91

Query Match          100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
Db      3 VKLAEEF 9
```


Db 3 VNLAAEF 9
|:::|

RESULT 165

US-11-090-399-92
; Sequence 92, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-92

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 3 VKLLAAEF 9

RESULT 166

US-11-090-399-93
; Sequence 93, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10

; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-93

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 3 VKFAAEF 9

RESULT 167

US-11-090-399-94
; Sequence 94, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-94

Query Match 100.0%; Score 7; DB 20; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0;

QY 1 VXXXAEF 7
|::|||
Db 3 VNFAAEF 9

RESULT 168

US-11-090-399-95
; Sequence 95, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-95

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|::|||
Db 3 VKFLAEF 9

RESULT 169

US-11-090-399-96
; Sequence 96, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APP fragment
US-11-090-399-96

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|::|||
Db 3 VNFLAEF 9

RESULT 170

US-11-042-695-8
; Sequence 8, Application US/11042695
; Publication No. US20050203096A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michael
; TITLE OF INVENTION: Compounds to Treat Alzheimer's Disease
; FILE REFERENCE: 01-1693-CC
; CURRENT APPLICATION NUMBER: US/11/042,695
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 09/895943
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-042-695-8

Query Match 100.0%; Score 7; DB 20; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|::|||
Db 3 VNLDAEF 9

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RESULT 171
US-11-074-828-10
; Sequence 10, Application US/11074828
; Publication No. US20050239832A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: MAILLARD, MICHEL
; APPLICANT: FANG, LAWRENCE
; APPLICANT: TUCKER, JOHN
; APPLICANT: BROGLEY, LOUIS
; APPLICANT: AQUINO, JOSE
; APPLICANT: BOWERS, SIMEON
; APPLICANT: PROBST, GARY
; APPLICANT: TUNG, JAY
; TITLE OF INVENTION: METHODS OF TREATMENT OF AMYLOIDOSIS USING BI-CYCLIC ASPARTYL PROTEASE INHIBITORS
; FILE REFERENCE: 09511.0007-00000
; CURRENT APPLICATION NUMBER: US/11/074,828
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,051
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/551,050
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/575,828
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/576,008
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/591,966
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/591,926
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/614,059
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/614,034
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-074-828-10
; Query Match 100.0%; Score 7; DB 20; Length 9;
; Best Local Similarity 57.1%; Pred. No. 1.7e+06;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEP 7
DB 3 VNLDAAEF 9

RESULT 172
US-11-075-294-10
; Sequence 10, Application US/11075294
; Publication No. US20050239790A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: MAILLARD, MICHEL
; APPLICANT: TUCKER, JOHN
; APPLICANT: JAGODZINSKA, BARBARA
; APPLICANT: BROGLEY, LOUIS
; APPLICANT: TUNG, JAY
; APPLICANT: SHAH, NEERAV
; APPLICANT: NEITZ, R. JEFFREY
; TITLE OF INVENTION: SUBSTITUTED HYDROXYETHYLAMINE ASPARTYL PROTEASE INHIBITORS
; FILE REFERENCE: 09511.0009-00000
; CURRENT APPLICATION NUMBER: US/11/075,294
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,296
; PRIOR FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,052
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/575,977
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/591,918
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/619,918
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-075-294-10
; Query Match 100.0%; Score 7; DB 20; Length 9;
; Best Local Similarity 57.1%; Pred. No. 1.7e+06;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEP 7
DB 3 VNLDAAEF 9

RESULT 173
US-11-075-312-10
; Sequence 10, Application US/11075312
; Publication No. US20050239836A1
; GENERAL INFORMATION:
; APPLICANT: JOHN, VARGHESE
; APPLICANT: MAILLARD, MICHEL
; APPLICANT: TUCKER, JOHN
; APPLICANT: AQUINO, JOSE
; APPLICANT: JAGODZINSKA, BARBARA
; APPLICANT: BROGLEY, LOUIS
; APPLICANT: TUNG, JAY
; APPLICANT: BOWERS, SIMEON
; APPLICANT: DRESSEN, DARREN
; APPLICANT: PROBST, GARY
; APPLICANT: SHAH, NEERAV
; TITLE OF INVENTION: SUBSTITUTED HYDROXYETHYLAMINE ASPARTYL PROTEASE INHIBITORS
; FILE REFERENCE: 09511.0008-00000
; CURRENT APPLICATION NUMBER: US/11/075,312
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: 60/551,052
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/575,977
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/591,918
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 60/619,918
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-075-312-10
; Query Match 100.0%; Score 7; DB 20; Length 9;
; Best Local Similarity 57.1%; Pred. No. 1.7e+06;
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEP 7
DB 3 VNLDAAEF 9
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```
RESULT 174
US-09-794-927-63
; Sequence 63, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-63

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 175
US-09-794-927-64
; Sequence 64, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-64

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 176
US-09-795-847-63
; Sequence 63, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-63

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 177
US-09-795-847-64
; Sequence 64, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
```

APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-64

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
DB 3 VNMDAEF 9

RESULT 178
US-09-794-743-63
; Sequence 63, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-63

Query Match 100.0%; Score 7; DB 9; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEF 7
|:::|
DB 3 VNMDAEF 9
RESULT 179
US-09-794-743-64
; Sequence 64, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-64

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
DB 3 VNMDAEF 9

RESULT 180
US-09-794-748-63
; Sequence 63, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-63

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```

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VXXAAEF 7
   |::|||
DB 3 VNLDAEF 9

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RESULT 181

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US-09-794-748-64
; Sequence 64, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:

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; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-64

```

```

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VXXAAEF 7
   |::|||
DB 3 VNLDAEF 9

```

RESULT 182

```

US-09-796-264-4
; Sequence 4, Application US/09796264

```

```

; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-796-264-4

```

```

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VXXAAEF 7
   |::|||
DB 3 VNLDAEF 9

```

RESULT 183

```

US-09-796-264-5
; Sequence 5, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-796-264-5

```

```
Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
       |:::|
Db      3 VNLDAEF 9

RESULT 184
US-09-794-925-63
; Sequence 63, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-63

Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
       |:::|
Db      3 VNLDAEF 9

RESULT 185
US-09-794-925-64
; Sequence 64, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
```

```
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-64

Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
       |:::|
Db      3 VNLDAEF 9

RESULT 186
US-09-681-442-63
; Sequence 63, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-63

Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXXAEF 7
       |:::|
Db      3 VNLDAEF 9

RESULT 187
US-09-681-442-64
; Sequence 64, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Rigiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-64

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 188
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-845-226-5

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 190
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
```

```
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9

RESULT 189
US-09-845-226-5
; Sequence 5, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-845-226-5

Query Match          100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VNLDAEF 9

RESULT 190
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
```


; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-795-903A-4

Query Match

100.0%; Score 7; DB 9; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7

|||||

Db 3 VKMDAEF 9

RESULT 191

US-09-795-903A-5

; Sequence 5, Application US/09795903A

; Patent No. US20020164760A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Jordan J.N.

; APPLICANT: Lin, Xinli

; APPLICANT: Koelsch, Gerald

; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods

; TITLE OF INVENTION: of Use Thereof

; FILE REFERENCE: OMRF 179

; CURRENT APPLICATION NUMBER: US/09/795,903A

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/604,608

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: 60/168,060

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: 60/177,836

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/178,368

; PRIOR FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: 60/210,292

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-795-903A-5

Query Match

100.0%; Score 7; DB 9; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7

|||||

Db 3 VKMDAEF 9

RESULT 192

US-09-908-943A-19

; Sequence 19, Application US/09908943A

; Publication No. US20030017991A1

; GENERAL INFORMATION:

; APPLICANT: Yan, Riqiang

; APPLICANT: Tomasselli, Alfredo G.

; APPLICANT: Gurney, Mark E.

; APPLICANT: Emmons, Thomas L.

; APPLICANT: Bienkowski, Mike J.

; APPLICANT: Heinrikson, Robert L.

; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY

; FILE REFERENCE: 29915/00281A.US1

; CURRENT APPLICATION NUMBER: US/09/908,943A

; CURRENT FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 60/219,795

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: peptide sequence

US-09-908-943A-19

Query Match

100.0%; Score 7; DB 10; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7

|||||

Db 3 VKMDAEF 9

RESULT 193

US-09-908-943A-20

; Sequence 20, Application US/09908943A

; Publication No. US20030017991A1

; GENERAL INFORMATION:

; APPLICANT: Yan, Riqiang

; APPLICANT: Tomasselli, Alfredo G.

; APPLICANT: Gurney, Mark E.

; APPLICANT: Emmons, Thomas L.

; APPLICANT: Bienkowski, Mike J.

; APPLICANT: Heinrikson, Robert L.

; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY

; FILE REFERENCE: 29915/00281A.US1

; CURRENT APPLICATION NUMBER: US/09/908,943A

; CURRENT FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 60/219,795

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: peptide sequence

US-09-908-943A-20

Query Match

100.0%; Score 7; DB 10; Length 10;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAEF 7

|||||

Db 3 VKMDAEF 9

RESULT 194

US-09-908-943A-21

; Sequence 21, Application US/09908943A

; Publication No. US20030017991A1

; GENERAL INFORMATION:

; APPLICANT: Yan, Riqiang

; APPLICANT: Tomasselli, Alfredo G.

; APPLICANT: Gurney, Mark E.

; APPLICANT: Emmons, Thomas L.

; APPLICANT: Bienkowski, Mike J.

; APPLICANT: Heinrikson, Robert L.

```
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: MOD RES
; LOCATION: (5)
; OTHER INFORMATION: Nle
; US-09-908-943A-21
```

```
Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VXXAAEF 7
|::|||
Db 3 VNXDAEF 9
```

RESULT 195

```
US-09-908-943A-143
; Sequence 143, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; US-09-908-943A-143
```

```
Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VXXAAEF 7
|::|||
Db 3 VSYDAEF 9
```

RESULT 196

```
US-09-908-943A-144
; Sequence 144, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
```

```
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 144
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; US-09-908-943A-144
```

```
Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VXXAAEF 7
|::|||
Db 3 VSYEAEF 9
```

RESULT 197

```
US-09-869-414-63
; Sequence 63, Application US/09869414
; Publication No. US2003007726A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-869-414-63
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Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VXXAAEF 7
|::|||
Db 3 VNLDAEF 9
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RESULT 198

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US-09-869-414-64
; Sequence 64, Application US/09869414
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; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-869-414-64

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|::|||
Db 3 VMDAEF 9

RESULT 200

US-09-548-366-64
; Sequence 64, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-548-366-64

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|::|||
Db 3 VMDAEF 9

Search completed: November 15, 2005, 11:18:15
Job time : 120 secs

; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-869-414-64

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
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Db 3 VMDAEF 9

RESULT 199

US-09-548-366-63
; Sequence 63, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-548-366-63

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|::|||
Db 3 VMDAEF 9

Search completed: November 15, 2005, 11:18:15
Job time : 120 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:29 ; Search time 24 Seconds
(without alignments)
28.063 Million cell updates/sec

Title: SEQ59

Perfect score: 7

Sequence: 1 vxxxaef 7

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 7

Total number of hits satisfying chosen parameters: 957

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	33	2 S23094	beta-amyloid prote
2	7	100.0	38	2 A18955	class II histocomp
3	7	100.0	39	2 A32533	class II histocomp
4	7	100.0	55	2 AH1443	phage protein homo
5	7	100.0	57	2 A60045	Alzheimer's diseas
6	7	100.0	57	2 F60045	Alzheimer's diseas
7	7	100.0	57	2 D60045	Alzheimer's diseas
8	7	100.0	57	2 E60045	Alzheimer's diseas
9	7	100.0	57	2 G60045	Alzheimer's diseas
10	7	100.0	57	2 B60045	Alzheimer's diseas
11	7	100.0	59	2 C72534	hypothetical prote
12	7	100.0	61	2 F36853	A50L protein - var
13	7	100.0	63	2 C72170	A54L protein - var
14	7	100.0	63	2 G64007	hypothetical prote
15	7	100.0	64	2 T34792	probable transcrip
16	7	100.0	68	1 QQH5NB	hypothetical prote
17	7	100.0	68	2 B84267	hypothetical prote
18	7	100.0	68	2 T10161	hypothetical prote
19	7	100.0	70	2 G82833	hypothetical prote
20	7	100.0	76	2 A54252	omega-agatoxin III
21	7	100.0	76	2 D54252	omega-agatoxin III
22	7	100.0	76	2 B54252	omega-agatoxin III
23	7	100.0	76	2 PQ0113	hypothetical prote
24	7	100.0	76	2 C54252	omega-agatoxin III
25	7	100.0	76	2 A42335	omega-agatoxin III
26	7	100.0	77	2 E82407	hypothetical prote
27	7	100.0	78	2 H71922	acyl carrier prote
28	7	100.0	78	2 G64589	acyl carrier prote
29	7	100.0	82	2 PQ0438	Alzheimer's diseas

30	7	100.0	90	2 A70600	hypothetical prote
31	7	100.0	92	2 A34520	calcium-binding pr
32	7	100.0	94	2 T08058	aspartic proteinas
33	7	100.0	94	2 T08062	aspartic proteinas
34	7	100.0	95	2 T45170	hypothetical prote
35	7	100.0	98	2 S41562	hypothetical prote
36	7	100.0	100	2 T49043	hypothetical prote
37	7	100.0	107	2 A82653	hypothetical prote
38	7	100.0	108	2 C64490	hypothetical prote
39	7	100.0	109	1 TLBEWL	minor tail protein
40	7	100.0	109	2 C85817	hypothetical prote
41	7	100.0	109	2 D90969	probable minor tai
42	7	100.0	109	2 E90899	probable minor tai
43	7	100.0	109	2 D90997	probable minor tai
44	7	100.0	109	2 D90834	minor tail protein
45	7	100.0	109	2 C90768	probable minor tai

ALIGNMENTS

RESULT 1

S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; PMID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 100.0%; Score 7; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
|:|:|:|:
DB 3 VKMDAEF 9

RESULT 2

A18955
class II histocompatibility antigen HLA-DR alpha chain - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A18955
R;Wiman, K.; Claesson, L.; Rask, L.; Tragardh, L.; Peterson, P.A.
Biochemistry 21, 5351-5358, 1982
A;Title: Purification and partial amino acid sequence of papain-solubilized class II trypsin-inhibitory peptides from human HLA-DR antigens
A;Reference number: A90463; PMID:83075335; PMID:6816270
A;Accession: A18955
A;Molecule type: protein
A;Residues: 1-38 <WIM>
A;Cross-references: UNIPROT:Q7M2H6
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 7; DB 2; Length 38;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
|:|:|:|:
DB 6 VIIQAEF 12

RESULT 3

A32533
class II histocompatibility antigen 37-68 alpha chain - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
 C;Accession: A32533
 R;Puri, N.K.; Walker, I.D.; Brandon, M.R.
 J. Immunol. 139, 2996-3002, 1987
 A;Title: N-terminal amino acid sequence analyses of the alpha-and beta-polypeptides from
 A;Reference number: A92815; MUID:88034383; PMID:3478413
 A;Accession: A32533
 A;Molecule type: protein
 A;Residues: 1-39 <PUR>
 A;Cross-references: UNIPROT:Q7M2H5
 A;Note: 4-Val and 33-Asp were also found
 C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 7; DB 2; Length 39;
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 6 VIIQAEF 12

RESULT 4
 AH1443
 phage protein homolog lin0087 [imported] - Listeria innocua (strain Clip11262)
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AH1443
 R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloecher
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluetter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AH1443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-55 <GLA>
 A;Cross-references: UNIPROT:Q92FL7; GB:AL592022; PIDN:CAC95320.1; PID:G16412507; GSPDB:G
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin0087

Query Match 100.0%; Score 7; DB 2; Length 55;
 Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 18 VDKLAEF 24

RESULT 5
 A60045
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: A60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: A60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56125
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
 Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 18 VDKLAEF 24

Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 3 VKMDAEF 9

RESULT 6
 F60045
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C;Accession: F60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: F60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56127; NID:G1895; PIDN:CAA39592.1; PID:G1896
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
 Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 3 VKMDAEF 9

RESULT 7
 D60045
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: D60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: D60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56124
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
 Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 3 VKMDAEF 9

RESULT 8
 E60045
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C;Species: Ovis sp. (sheep)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: E60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: E60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56130

A;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

|:::|
Db 3 VKMDAEF 9

RESULT 9

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: G60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56126

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

|:::|
Db 3 VKMDAEF 9

RESULT 10

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C;Species: Ursus maritimus (polar bear)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: UNIPROT:Q29149; EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 7; DB 2; Length 57;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

|:::|
Db 3 VKMDAEF 9

RESULT 11

C72534

hypothetical protein AP05056 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: C72534

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: C72534

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-59 <KAW>

A;Cross-references: UNIPROT:Q9YBN8; DDBJ:AP000062; NID:g5105244; PIDN:BAA80560.1; PID:d

A;Experimental source: strain K1

C;Genetics:

A;Gene: AP05056

Query Match 100.0%; Score 7; DB 2; Length 59;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

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Db 53 VAFEAEF 59

RESULT 12

F36853

A50L protein - variola virus (strain India-1967)

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: F36853

R;Blinov, V.M.

submitted to GenBank, November 1992

A;Reference number: A36859

A;Accession: F36853

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-61 <BLI>

A;Cross-references: UNIPROT:P33794; GB:X69198; NID:g456758; PIDN:CAA49097.1; PID:g45704

Query Match 100.0%; Score 7; DB 2; Length 61;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

|:::|
Db 6 VTGGAEF 12

RESULT 13

C72170

A54L protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004

C;Accession: C72170

R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopa

submitted to GenBank, March 1998

A;Description: Analysis of the complete coding sequence of DNA of alastrim variola mino

A;Reference number: A72150

A;Accession: C72170

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-61 <SHC>

A;Cross-references: UNIPROT:Q9QNH1; GB:Y16780; NID:g5830555; PIDN:CAB54757.1; PID:e1542

A;Experimental source: strain Garcia-1966

C;Genetics:

A;Gene: A54L

Query Match 100.0%; Score 7; DB 2; Length 61;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7

|:::|
Db 6 VTGGAEF 12

```
RESULT 14
G64007
hypothetical protein HI0451 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: G64007
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64007
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-63 <TTGR>
A;Cross-references: UNIPROT:P43998; GB:U32728; GB:I42023; NID:gl573425; PIDN:AAC22109.1;
GSPDB:SC2E1.24

Query Match 100.0%; Score 7; DB 2; Length 63;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 24 VGEVAEF 30

RESULT 15
T34792
probable transcription regulator - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34792
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21557
A;Accession: T34792
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-64 <MUR>
A;Cross-references: UNIPROT:O69895; EMBL:AL023797; PIDN:CAA19399.1; GSPDB:GNO0070; SCOE
A;Experimental source: strain A3(2)
C:Genetics:
A;Gene: SCOE:SC2E1.24

Query Match 100.0%; Score 7; DB 2; Length 64;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 24 VELSAEF 30

RESULT 16
QOHSNB
hypothetical protein NAB - Halobacterium salinarum (strain cutirubrum)
C:Species: Halobacterium salinarum
A:Variety: strain cutirubrum
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S04117
R:Shimmin, L.C.; Dennis, P.P.
EMBO J. 8, 1225-1235, 1989
A;Title: Characterization of the L11, L1, L10 and L12 equivalent ribosomal protein gene
A;Reference number: S04116; MUID:89305527; PMID:2743981
A;Accession: S04117
A:Molecule type: DNA
A;Residues: 1-68 <SHI>
A;Cross-references: UNIPROT:P17104; EMBL:X15078; NID:g43449; PIDN:CAA33177.1; PID:g43451
A;Note: the source is designated as Halobacterium cutirubrum
C:Superfamily: hypothetical protein NAB
```

```
Query Match 100.0%; Score 7; DB 1; Length 68;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 25 VDLEAEF 31

RESULT 17
B84267
hypothetical protein Vngl110c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84267
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84267
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross-references: UNIPROT:P17104; GB:AE004437; NID:gl0580654; PIDN:AAG19502.1; GSPDB:
C:Genetics:
A;Gene: VNG110C
C:Superfamily: hypothetical protein NAB

Query Match 100.0%; Score 7; DB 2; Length 68;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 25 VDLEAEF 31

RESULT 18
T10161
hypothetical protein G - phage T4
C:Species: phage T4
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10161
R:Gram, H.; Ruger, W.
EMBO J. 4, 257-264, 1985
A;Title: Genes 55, alpha-gt, 47 and 46 of bacteriophage T4: the genomic organization as
A;Reference number: A91016; MUID:85257446; PMID:4018026
A;Accession: T10161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-68 <GRA>
A;Cross-references: UNIPROT:P32268; EMBL:X01804; NID:gl5229; PID:g577851

Query Match 100.0%; Score 7; DB 2; Length 68;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 39 VVCAAEF 45

RESULT 19
GB2833
hypothetical protein XF0219 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: GB2833
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
```


A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below

A;Accession: G82833

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-70 <SIM>

A;Cross-references: UNIPROT:Q9PGS9; GB:AE003875; GB:AE003849; NID:g9105019; PIDN:AAF8303

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincan, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0219

Query Match 100.0%; Score 7; DB 2; Length 70;

Best Local Similarity 57.1%; Pred.No. 2.9e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7

Db 6 VRKSAEF 12

RESULT 20

A54252

omega-agatoxin III, 8.478K - funnel-weaving spider (Agelenopsis aperta)

C;Species: Agelenopsis aperta

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996

C;Accession: A54252

R;Ertel, E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.

Biochemistry 33, 5098-5108, 1994

A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- a

A;Reference number: A54252; MUID:94227039; PMID:8172884

A;Accession: A54252

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-76 <ERT>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:148239)

Query Match 100.0%; Score 7; DB 2; Length 76;

Best Local Similarity 57.1%; Pred.No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7

Db 42 VGTSAEF 48

RESULT 21

D54252

omega-agatoxin III, 8.581K - funnel-weaving spider (Agelenopsis aperta)

C;Species: Agelenopsis aperta

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996

C;Accession: D54252

R;Ertel, E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.

Biochemistry 33, 5098-5108, 1994

A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- a

A;Reference number: A54252; MUID:94227039; PMID:8172884

A;Accession: D54252

A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-76 <ERT>
 A;Experimental source: venom
 A;Note: sequence extracted from NCBI backbone (NCBIP:148242)

Query Match 100.0%; Score 7; DB 2; Length 76;

Best Local Similarity 57.1%; Pred.No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7

Db 42 VGTSAEF 48

RESULT 22

B54252

omega-agatoxin III, 8.637K - funnel-weaving spider (Agelenopsis aperta)

C;Species: Agelenopsis aperta

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996

C;Accession: B54252

R;Ertel, E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.

Biochemistry 33, 5098-5108, 1994

A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- a

A;Reference number: A54252; MUID:94227039; PMID:8172884

A;Accession: B54252

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-76 <ERT>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:148240)

Query Match 100.0%; Score 7; DB 2; Length 76;

Best Local Similarity 57.1%; Pred.No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7

Db 42 VGTSAEF 48

RESULT 23

PQ0113

hypothetical protein (hisa 3' region) - Streptomyces coelicolor (fragment)

C;Species: Streptomyces coelicolor

C;Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: PQ0113

R;Limauro, D.; Avitabile, A.; Cappellano, C.; Puglia, A.M.; Bruni, C.B.

Gene 90, 31-41, 1990

A;Title: Cloning and characterization of the histidine biosynthetic gene cluster of Str

A;Reference number: JQ0637; MUID:90337345; PMID:2199329

A;Accession: PQ0113

A;Molecule type: DNA

A;Residues: 1-76 <LIM>

A;Cross-references: UNIPROT:P16251; GB:M31628; NID:g153295; PIDN:AAA26761.1; PID:g15330

Query Match 100.0%; Score 7; DB 2; Length 76;

Best Local Similarity 57.1%; Pred.No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7

Db 62 VEAIAEF 68

RESULT 24

C54252

omega-agatoxin III, 8.607K - funnel-weaving spider (Agelenopsis aperta)

C;Species: Agelenopsis aperta

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: C54252

R;Ertel, E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.

Biochemistry 33, 5098-5108, 1994

A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- a

```

A;Reference number: A54252; MUID:94227039; PMID:8172884
A;Accession: C54252
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-76 <ERT>
A;Cross-references: UNIPROT:P81744
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148241)

Query Match      100.0%; Score 7; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 42 VGTSAEEF 48

RESULT 25
A42335
omega-agatoxin IIIA - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42335
R;Venema, V.J.; Swiderek, K.M.; Lee, T.D.; Hathaway, G.M.; Adams, M.E.
J. Biol. Chem. 267, 2610-2615, 1992
A;Title: Antagonism of synaptosomal calcium channels by subtypes of omega-agatoxins.
A;Reference number: A42335; MUID:92129351; PMID:1310319
A;Accession: A42335
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-76 <VEN>
A;Cross-references: UNIPROT:P33034
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:78693)

Query Match      100.0%; Score 7; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 42 VGTSAEEF 48

RESULT 26
E82407
hypothetical protein VCA0868 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82407
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 405, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82407
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-77 <HEI>
A;Cross-references: UNIPROT:Q9KL79; GB:AE004414; GB:AE003853; NID:g9658293; PIDN:AAF9676
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0868
A;Map position: 2

Query Match      100.0%; Score 7; DB 2; Length 77;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 42 VGTSAEEF 48

A;Reference number: A54252; MUID:94227039; PMID:8172884
A;Accession: C54252
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-76 <ERT>
A;Cross-references: UNIPROT:P81744
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148241)

Query Match      100.0%; Score 7; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 42 VGTSAEEF 48

RESULT 27
H71922
acyl carrier protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: H71922
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: H71922
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-78 <ARN>
A;Cross-references: UNIPROT:Q9ZLS1; GB:AE001484; GB:AE001439; NID:g4155043; PIDN:AAD060
A;Experimental source: strain J99
C;Genetics:
A;Gene: acpP
C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;1-72/Domain: acyl carrier protein homology <ACP>
F;36/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match      100.0%; Score 7; DB 2; Length 78;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 22 VTPEAEEF 28

RESULT 28
G64589
acyl carrier protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: G64589
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64589
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-78 <DGM>
A;Cross-references: UNIPROT:P56464; GB:AE000570; GB:AE000511; NID:g2313672; PIDN:AAD076
C;Genetics:
A;Gene: acpP
C;Function:
A;Description: carrier of the growing fatty acid chain; growing fatty acid chain is cov.
A;Pathway: fatty acid biosynthesis
C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C;Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein;
F;1-72/Domain: acyl carrier protein homology <ACP>
F;36/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match      100.0%; Score 7; DB 2; Length 78;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 22 VTPEAEEF 28

```

RESULT 29

PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C;Accession: PQ0438; C60045
 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A;Reference number: PQ0438; MUID:93075180; PMID:1445331
 A;Accession: PQ0438
 A;Molecule type: DNA
 A;Residues: 1-82 <DAV>
 A;Cross-references: GB:M83558; GB:M83657
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: C60045
 A;Molecule type: mRNA
 A;Residues: 12-68 <JOH>
 A;Cross-references: EMBL:X56129
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 7; DB 2; Length 82;
 Best Local Similarity 57.1%; Pred. No. 3.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 14 VKMDAEF 20

RESULT 30

A70600
 hypothetical protein Rv3904c - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: A70600
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: A70600
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-90 <COL>
 A;Cross-references: UNIPROT:O05441; GB:Z94121; GB:AL123456; NID:g3261736; PIDN:CAB08097.
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: Rv3904c

Query Match 100.0%; Score 7; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 3.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 10 VARMAEF 16

RESULT 31

A34520
 calcium-binding protein, vitamin D-dependent - guinea pig (fragments)
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
 C;Accession: A34520
 R;Winsky, L.; Nakata, H.; Martin, B.M.; Jacobowitz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 10139-10143, 1989
 A;Title: Isolation, partial amino acid sequence, and immunohistochemical localization o
 A;Reference number: A34520; MUID:90099311; PMID:2602362
 A;Accession: A34520
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-92 <WIN>

A;Cross-references: UNIPROT:P20658
 C;Superfamily: calretinin; calmodulin repeat homology
 C;Keywords: brain; calcium binding; duplication; EF hand; vitamin D

Query Match 100.0%; Score 7; DB 2; Length 92;
 Best Local Similarity 57.1%; Pred. No. 3.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 30 VGSSAEF 36

RESULT 32

T08058
 aspartic proteinase inhibitor - winter squash (fragment)
 C;Species: Cucurbita maxima (winter squash)
 C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C;Accession: T08058
 R;Christeller, J.T.; Farley, P.C.; Ramsay, R.J.; Sullivan, P.A.; Laing, W.A.
 Eur. J. Biochem. 254, 160-167, 1998
 A;Title: Purification, characterization and cloning of an aspartic proteinase inhibitor
 A;Reference number: Z16322; MUID:98314517; PMID:9652409
 A;Accession: T08058
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-94 <CHR>
 A;Cross-references: UNIPROT:O81131; EMBL:AF038166; NID:g3236358; PIDN:AAC39473.1; PID:g
 C;Genetics:
 A;Gene: API-1

Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 3.7e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 18 VKEIAEF 24

RESULT 33

T08062
 aspartic proteinase inhibitor 2 - winter squash (fragment)
 C;Species: Cucurbita maxima (winter squash)
 C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C;Accession: T08062
 R;Christeller, J.T.; Farley, P.C.; Ramsay, R.J.; Sullivan, P.A.; Laing, W.A.
 Eur. J. Biochem. 254, 160-167, 1998
 A;Title: Purification, characterization and cloning of an aspartic proteinase inhibitor
 A;Reference number: Z16322; MUID:98314517; PMID:9652409
 A;Accession: T08062
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-94 <CHR>
 A;Cross-references: UNIPROT:O81132; EMBL:AF038167; NID:g3236360; PIDN:AAC39474.1; PID:g
 C;Genetics:
 A;Gene: API-2

Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 3.7e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 18 VKEIAEF 24

```

RESULT 34
T45170
hypothetical protein u1756d [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45170
submitted to the EMBL Data Library, September 1994
R:Robison, K.
A:Reference number: Z16911
A:Accession: T45170
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <KEI>
A:Cross-references: UNIPROT:Q49946; EMBL:U15180; PIDN:AAA62302.1

Query Match 100.0%; Score 7; DB 2; Length 95;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 36 VRDAEF 42
|::|||

RESULT 35
S41562
hypothetical protein bglA 5'-region - Thermotoga maritima
C:Species: Thermotoga maritima
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41562; S34571
R:Liebl, W.; Gabelsberger, J.; Schleifer, K.H.
Mol. Gen. Genet. 242, 111-115, 1994
A:Title: Comparative amino acid sequence analysis of Thermotoga maritima beta-glucosidases of the BGA family and other families of beta-1,4-glycosyl hydrolases.
A:Reference number: S41561; MUID:94104595; PMID:8277941
A:Accession: S41562
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <LE>
A:Cross-references: UNIPROT:Q08640; EMBL:X74163; NID:G3952290; PIDN:CAAS52277.1; PID:G3952
A:Experimental source: strain MS88
C:Comment: This is the hypothetical translation of a sequence that was not reported as a nucleotide sequence for this region, see also PIR:S34570, was not found.

Query Match 100.0%; Score 7; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 86 VIWPAEF 92
|::|||

RESULT 36
T49043
hypothetical protein T5p19.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49043
R:Benes, V.; Wurmbach, B.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25014
A:Accession: T49043
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <BEN>
A:Cross-references: UNIPROT:Q9LXZ8; EMBL:AL163372; GSPDB:GN00061; ATSP:T5P19.70
A:Experimental source: cultivar Columbia; EAC clone T5P19
C:Genetics:
A:Gene: ATSP:T5P19.70
A:Map position: 3
A:Introns: 16/2; 51/3

```

```

Query Match 100.0%; Score 7; DB 2; Length 100;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 47 VEELAEF 53
|::|||

RESULT 37
AB2653
hypothetical protein XP1662 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: AB2653
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB2515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: AB2653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <SIM>
A:Cross-references: UNIPROT:Q9PCU3; GB:AE003932; GB:AE003849; NID:G9106715; PIDN:AAF844
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, I.; as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohlich, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigachado, M.A.; Madeira, E.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; SawasakRodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; SawasakM.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XP1662

Query Match 100.0%; Score 7; DB 2; Length 107;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 86 VLFGAEF 92
|::|||

RESULT 38
C64490
hypothetical protein MJ1524 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64490
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A., rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64490
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <BUL>
A:Cross-references: UNIPROT:Q58919; GB:U67593; GB:L77117; NID:G2826427; PIDN:AAB99550.1;
C:Genetics:
A:Map position: FOR1501406-1501732

```

C;Superfamily: uncharacterized conserved protein MJ1524

Query Match 100.0%; Score 7; DB 2; Length 108;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 49 VRGVAEF 55

RESULT 39

TLBPML

minor tail protein M - phage lambda

C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: I43008; F43014; A04363

R;Daniels, D.

submitted to the Nucleic Acid Sequence Database, September 1982

A;Reference number: A94614

A;Accession: I43008

A;Molecule type: DNA

A;Residues: 1-109 <DAN>

A;Cross-references: UNIPROT:P03737

R;Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.

J. Mol. Biol. 162, 729-773, 1982

A;Title: Nucleotide sequence of bacteriophage lambda DNA.

A;Reference number: A92891; MUID:83189071; PMID:6221115

A;Accession: F43014

A;Molecule type: DNA

A;Residues: 1-109 <SAN>

A;Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:G215104;

A;Note: the codon corresponding to 1-Met is the most probable of five possible translations

C;Comment: Gene M protein is a minor tail protein, located at the distal end, and is involved in

C;Genetics:

A;Gene: M

A;Map position: 27.01-27.68

C;Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 1; Length 109;

Best Local Similarity 57.1%; Pred. No. 4.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 98 VEFSAEF 104

RESULT 40

C85817

hypothetical protein Z3083 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 18-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: C85817; C85718

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: C85817

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <STO>

A;Cross-references: UNIPROT:Q9EYE2; UNIPROT:Q8FIG1; GB:AE005174; NID:g12516100; PIDN:AAG

A;Experimental source: strain O157:H7, substrain EDL933

A;Accession: C85718

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <ST2>

A;Cross-references: GB:AE005174; NID:g12515095; PIDN:AAG56207.1; GSPDB:GN00145; UWGP:Z21

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z3083; Z2141

C;Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 98 VEFSAEF 104

RESULT 41

D90969

probable minor tail protein [imported] - Escherichia coli (strain O157:H7, substrain RI

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: D90969

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D90969

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <HAY>

A;Cross-references: UNIPROT:Q9EYE2; UNIPROT:Q8FIG1; GB:BA000007; PIDN:BAB36147.1; PID:9

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs2724

C;Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;

Best Local Similarity 57.1%; Pred. No. 4.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 98 VEFSAEF 104

RESULT 42

E90899

probable minor tail protein [imported] - Escherichia coli (strain O157:H7, substrain RI

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: E90899

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: E90899

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <HAY>

A;Cross-references: UNIPROT:Q9EYE2; UNIPROT:Q8FIG1; GB:BA000007; PIDN:BAB35588.1; PID:9

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs2165

C;Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;

Best Local Similarity 57.1%; Pred. No. 4.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 98 VEFSAEF 104

RESULT 43

D90997

```

probable minor tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D90997
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90997
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <HAY>
A:Cross-references: UNIPROT:Q9EY22; UNIPROT:Q9FIG1; GB:BA000007; PIDN:BA036371.1; PID:gl
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2948
C:Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 98 VEFSAEF 104

RESULT 44
D90834
minor tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D90834
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90834
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <HAY>
A:Cross-references: UNIPROT:Q8X305; GB:BA000007; PIDN:BA035067.1; PID:gl13361108; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1644
C:Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 98 VEFSAEF 104

RESULT 45
C90768
probable minor tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90768
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90768
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <HAY>

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A:Cross-references: UNIPROT:Q8X4W8; GB:BA000007; PIDN:BA034538.1; PID:gl13360575; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1115
C:Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 98 VEFSAEF 104

RESULT 46
C85742
probable tail component of prophage CP-933R Z2353 [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85742
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85742
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <STO>
A:Cross-references: UNIPROT:Q8X4W8; GB:AE005174; NID:gl2515345; PIDN:AAG56399.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z2353
C:Superfamily: phage lambda minor tail protein M

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 98 VEFSAEF 104

RESULT 47
C75150
hypothetical protein PAB0239 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75150
R:anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: C75150
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <KAW>
A:Cross-references: UNIPROT:Q9V1R7; GB:AJ248284; GB:AL096836; NID:gs457730; PIDN:CAB492
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0239
C:Superfamily: conserved hypothetical protein H11297

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 49 VEKEAEF 55

```

RESULT 48

A71191
hypothetical protein PH1801 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: A71191
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71191
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-109 <KAW>
A;Cross-references: UNIPROT:O59465; GB:AP000007; NID:g3236134; PIDN:BAA30920.1; PID:g325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1801

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 49 VEREAEF 55

RESULT 49

T45387
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45387
R;Cole, S.T.; Flesselles, B.; Honore, N.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z22966
A;Accession: T45387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-110 <COL>
A;Cross-references: UNIPROT:Q33004; EMBL:Z98756; PIDN:CAB11457.1
A;Experimental source: cosmid B2492
C;Genetics:
A;Note: MLCB2492.25

Query Match 100.0%; Score 7; DB 2; Length 110;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 92 VGEAEF 98

RESULT 50

F87476
hypothetical protein CC1835 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87476
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87476
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-111 <STO>

A;Cross-references: UNIPROT:Q9A791; GB:AE005673; NID:g13423274; PIDN:AAK23810.1; GSPDB:
C;Genetics:
A;Gene: CC1835

Query Match 100.0%; Score 7; DB 2; Length 111;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 12 VLYAEF 18

RESULT 51

D96748
hypothetical protein T10D10.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96748
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: UNIPROT:Q9C9E1; GB:AE005173; NID:g6730758; PIDN:AAF27147.1; GSPDB:G
C;Genetics:
A;Gene: T10D10.10
A;Map position: 1

Query Match 100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 110 VEELAEF 116

RESULT 52

S48420
probable membrane protein Y1L059c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48420
R;Smith, V.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48407
A;Accession: S48420
A;Molecule type: DNA
A;Residues: 1-121 <SMI>
A;Cross-references: UNIPROT:P40520; GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763287; G
C;Genetics:
A;Gene: MIPS:Y1L059c
A;Cross-references: SGD:S0001321
A;Map position: 9L
C;Superfamily: Saccharomyces probable membrane protein Y1L059c
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 7; DB 2; Length 121;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 19 VTAAEF 25

RESULT 53

S58332
hypothetical protein orf 6150 - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1996 #sequence_revision 05-Sep-1996 #text_change 09-Jul-2004
C:Accession: S58332
R:Pearson, B.M.; Hernandez, Y.; Payne, J.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
Yeast 12, 1021-1031, 1996
A:Title: Sequencing of a 35.71 kb DNA segment on the right arm of yeast chromosome XV re
A:Reference number: S71986; MUID:97051589; PMID:8896266
A:Accession: S72002
A:Status: nucleic acid sequence not shown; translation not shown; conceptual translation
A:Molecule type: DNA
A:Residues: 1-121 <PEA>
A:Cross-references: UNIPROT:Q05388; EMBL:X90565; NID:g940836; PIDN:CAA62177.1; PID:g9408
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C:Comment: There is no evidence that this sequence is expressed.
C:Genetics:
A:Map position: 15R
C:Keywords: pseudogene

Query Match 100.0%; Score 7; DB 4; Length 121;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 55 VAIIAEF 61

RESULT 54

H63292
desulfotetrodotoxin homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H63292
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: H63292
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-125 <KLE>
A:Cross-references: UNIPROT:Q29903; GB:AE001081; GB:AE000782; NID:g2689404; PIDN:AAB9089
C:Superfamily: superoxide reductase/superoxide dismutase; desulfotetrodotoxin homology

Query Match 100.0%; Score 7; DB 2; Length 125;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 65 VVGAEEF 71

RESULT 55

S76031
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76031

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

s.
A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76031
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-131 <KAN>
A:Cross-references: UNIPROT:Q55519; EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAAL08.
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG
C:Superfamily: hypothetical protein sll1092

Query Match 100.0%; Score 7; DB 2; Length 131;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 69 VKLGAEEF 75

RESULT 56

A86310
F28G4.20 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86310
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huiziar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Mafti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86310
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <STO>
A:Cross-references: UNIPROT:Q9LQ16; GB:AE005172; NID:g9665126; PIDN:AAF97310.1; GSPDB:GN

C:Genetics:
A:Map position: 1
Query Match 100.0%; Score 7; DB 2; Length 131;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 122 VEELAEF 128

RESULT 57

JQ0737
RnpA protein - Micrococcus luteus
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: JQ0737
R:Fujita, M.Q.; Yoshikawa, H.; Ogasawara, N.
Gene 93, 73-78, 1990
A:Title: Structure of the dnaA region of Micrococcus luteus: conservation and variation
A:Reference number: JQ0737; MUID:91033019; PMID:2172090
A:Accession: JQ0737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <FUJ>

A;Cross-references: UNIPROT:P21172; GB:M34006; NID:g149845; PIDN:AAA25313.1; PID:g455290
C;Superfamily: ribonuclease P, protein component

Query Match 100.0%; Score 7; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 8 VRTPAEF 14

RESULT 58

T35078
conserved hypothetical protein SC4G6.18c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T35078
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21567

A;Accession: T35078
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-134 <SEE>

A;Cross-references: UNIPROT:P16251; EMBL:AL096884; PIDN:CAB51441.1; GSPDB:GN000070; SCORE
A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SC0EDB:SC4G6.18c

Query Match 100.0%; Score 7; DB 2; Length 134;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 62 VEAIAEF 68

RESULT 59

H81290
hypothetical protein Cj1449c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81290

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrer

Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: H81290

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-135 <PAR>

A;Cross-references: UNIPROT:Q9PML1; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7387
A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj1449c

C;Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 7; DB 2; Length 135;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 77 VQAKAEF 83

RESULT 60

T08296
hypothetical protein H0911 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100
C;Species: Halobacterium sp.

A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08296

R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baekin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998

A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or

A;Reference number: Z16408; MUID:99063795; PMID:9847077

A;Accession: T08296

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-140 <DAS>

A;Cross-references: UNIPROT:O51983; EMBL:AF016485; NID:g2822278; PID:g2822357; HALOSP:H
A;Experimental source: strain NRC-1

C;Genetics:

A;Gene: HALOSP:H0911

A;Genome: plasmid pNRC100

Query Match 100.0%; Score 7; DB 2; Length 140;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 94 VELKAEF 100

RESULT 61

S52305

heat shock transcription factor 33 pseudogene - soybean

C;Species: Glycine max (soybean)

C;Date: 08-May-1995 #sequence_revision 18-Jan-1996 #text_change 17-Mar-1996
C;Accession: S52305

R;Czarnecka-Verner, E.; Yuan, C.X.; Fox, P.C.; Gurley, W.B.

submitted to the EMBL Data Library, December 1994

A;Description: Isolation and characterization of six heat shock transcription factor cd

A;Reference number: S52303

A;Accession: S52305

A;Status: conceptual translation of pseudogene

A;Molecule type: mRNA

A;Residues: 1-142 <CZA>

A;Cross-references: EMBL:Z46954

C;Keywords: pseudogene

Query Match 100.0%; Score 7; DB 4; Length 142;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|
Db 6 VWRPAEF 12

RESULT 62

C87022

conserved hypothetical protein ML0905 [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: C87022

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: C87022

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-143 <STO>

A;Cross-references: UNIPROT:O69561; GB:AL450380; NID:g13092975; PIDN:CAC31286.1; GSPDB:

C;Genetics:

A;Gene: ML0905

C;Superfamily: hypothetical protein MG221

Query Match 100.0%; Score 7; DB 2; Length 143;
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 42 VYPRAEF 48

RESULT 63
 AF2781
 hypothetical protein Atul668 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AF2781
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:AuthorB: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AF2781
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <RUR>
 A:Cross-references: UNIPROT:Q8UET7; GB:AE008688; PIDN:AAL42668.1; PID:g17740101; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atul668
 A:Map position: circular chromosome

Query Match 100.0%; Score 7; DB 2; Length 143;
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 93 VQQAEEF 99

RESULT 64
 S53712
 nitric-oxide reductase (EC 1.7.99.7) cytochrome c chain - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S53712; G83579
 R:Arai, H.; Igarashi, Y.; Kodama, T.
 Biochim. Biophys. Acta 1261, 279-284, 1995
 A>Title: The structural genes for nitric oxide reductase from Pseudomonas aeruginosa.
 A:Reference number: S53712; MUID:95226457; PMID:7711073
 A:Accession: S53712
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <ARA>
 A:Cross-references: UNIPROT:Q59646; EMBL:D38133; NID:g537365; PIDN:BAA07329.1; PID:d1007
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: AB2950; MUID:20437337; PMID:10984043
 A:Accession: G83579
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <STO>
 A:Cross-references: GB:AE004489; GB:AE004091; NID:g9946385; PIDN:AAG03912.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: norC; PA0523
 C:Superfamily: nitric-oxide reductase cytochrome c subunit

C:Keywords: oxidoreductase

Query Match 100.0%; Score 7; DB 2; Length 146;
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 122 VDDLAEF 128

RESULT 65

S41116
 nitric-oxide reductase (EC 1.7.99.7) cytochrome c chain - Pseudomonas stutzeri
 C:Species: Pseudomonas stutzeri
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S41116
 R:Tumft, W.G.; Braun, C.; Cuypers, H.
 Eur. J. Biochem. 219, 481-490, 1994
 A>Title: Nitric oxide reductase from Pseudomonas stutzeri. Primary structure and gene o
 A:Reference number: S41116; MUID:94139726; PMID:7508388
 A:Accession: S41116
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <ZUM>
 A:Cross-references: UNIPROT:Q52527; EMBL:Z28384; NID:g433604; PIDN:CAA82228.1; PID:g433
 C:Superfamily: nitric-oxide reductase cytochrome c subunit
 C:Keywords: oxidoreductase

Query Match 100.0%; Score 7; DB 2; Length 146;
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 122 VDDMAEF 128

RESULT 66

C64636
 hypothetical protein HP0931 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64636
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64636
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-146 <TOM>
 A:Cross-references: UNIPROT:Q25585; GB:AE000602; GB:AE000511; NID:g2314050; PIDN:AAD079
 C:Genetics:
 A:Start codon: GTG

Query Match 100.0%; Score 7; DB 2; Length 146;
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 77 VFTQAEF 83

RESULT 67

H84341
 hypothetical protein Vng1907h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84341
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: H84341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <STO>
A;Cross-references: UNIPROT:Q9HNX0; GB:AE004437; NID:g10581349; PIDN:AAG20100.1; GSPDB:G
C;Genetics:
A;Gene: VNG1907H

Query Match 100.0%; Score 7; DB 2; Length 147;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 102 VSSRAEF 108

RESULT 68
E81788
conserved hypothetical protein NMA2160 [imported] - Neisseria meningitidis (strain Z2491)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
A;Accession: E81788
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81788
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <PAR>
A;Cross-references: UNIPROT:Q9JSS2; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8537
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2160
C;Superfamily: hypothetical protein ytwI

Query Match 100.0%; Score 7; DB 2; Length 148;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 74 VPPVAEF 80

RESULT 69
A85878
non-heme iron-binding ferritin [imported] - Lactococcus lactis subsp. lactis (strain IL1
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
A;Accession: A86878
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mialme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <STO>
A;Cross-references: UNIPROT:Q9CE23; GB:AE005176; PID:g12725073; PIDN:AAK06123.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: dpsA

C;Superfamily: hypothetical protein H11349

Query Match 100.0%; Score 7; DB 2; Length 148;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 69 VSTLAEEF 75

RESULT 70
F97205
hypothetical protein CAC2479 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
A;Accession: F97205
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97205
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <KUR>
A;Cross-references: UNIPROT:Q97G90; GB:AE001437; PIDN:AAK80433.1; PID:g15025499; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2479

Query Match 100.0%; Score 7; DB 2; Length 148;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 32 VNERAEF 38

RESULT 71
S22328
gene D protein - phage alpha-3
C;Species: phage alpha-3
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
A;Accession: S22328; S07299
R;Kodaira, K.I.; Nakano, K.; Okada, S.; Taketo, A.
Biochim. Biophys. Acta 1130, 277-288, 1992
A;Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationsh
A;Reference number: S22324; MUID:92223109; PMID:1532908
A;Accession: S22328
A;Molecule type: DNA
A;Residues: 1-150 <KOD>
A;Cross-references: UNIPROT:P08765; EMBL:X60322; NID:g14775; PIDN:CAA42878.1; PID:g1478
R;Kodaira, K.I.; Taketo, A.
Mol. Gen. Genet. 195, 541-543, 1984
A;Title: Isolation and some properties of bacteriophage alpha3 gene J mutant.
A;Reference number: S07299; MUID:84294906; PMID:6088949
A;Accession: S07299
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 114-117, 'P', 118, 'R', 121-150 <KOD>
A;Cross-references: EMBL:X00774; NID:g15431; PIDN:CAA25348.1; PID:g15432
C;Genetics:
A;Gene: D
C;Superfamily: phage phi-X174 gene D protein

Query Match 100.0%; Score 7; DB 2; Length 150;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|

Db 95 VMEGAEP 101

RESULT 72

G84585

probable kinetechore (Skp1p-like) protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: G84585

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84585

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-150 <STO>

A:Cross-references: UNIPROT:Q9SL65; GB:AE002093; NID:g4580458; PIDN:AAD24382.1; GSPDB:GN

C:Genetics:

A:Gene: At2g20160

A:Map position: 2

C:Superfamily: human S-phase kinase-associated protein 1A

Query Match 100.0%; Score 7; DB 2; Length 150;

Best Local Similarity 57.1%; Pred. No. 5.4e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

Db 73 VTWDAEP 79

RESULT 73

T12249

major latex protein homolog - common ice plant

C:Species: Mesembryanthemum crystallinum (Common ice plant)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004

C:Accession: T12249

R:Michalowski, C.B.; Bohnert, H.J.

submitted to the EMBL Data Library, March 1998

A:Description: A wound-induced protein homolog from M. crystallinum.

A:Reference number: Z17472

A:Accession: T12249

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-152 <MIC>

A:Cross-references: UNIPROT:O65178; EMBL:AF054445; NID:g3064038; PID:g3064039

C:Superfamily: wound-induced protein Sn-1

Query Match 100.0%; Score 7; DB 2; Length 152;

Best Local Similarity 57.1%; Pred. No. 5.5e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

Db 114 VRWIAEP 120

RESULT 74

A49241

superoxide dismutase (EC 1.15.1.1) (Cu-Zn), cytosolic - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C:Accession: A49241

R:Hong, Z.; LoVerde, P.T.; Hammarckjold, M.L.; Rekosh, D.

Exp. Parasitol. 75, 308-322, 1992

A:Title: Schistosoma mansoni: cloning of a complementary DNA encoding a cytosolic Cu/Zn

A:Reference number: A49241; MUID:93050040; PMID:1426133

A:Accession: A49241

A>Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-153 <HON>

A:Cross-references: UNIPROT:Q01137; GB:M97298; NID:g161118; PIDN:AAA29935.1; PID:g16111

A>Note: sequence extracted from NCBI backbone (NCBIN:118959, NCBIP:118960)

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: Superoxide dismutase [Cu-Zn]

C:Keywords: copper; cytosol; metalloprotein; oxidoreductase; zinc

F:45,47,62,119/Binding site: copper (His) #status predicted

F:56-145/Disulfide bonds: #status predicted

F:62,70,79,82/Binding site: zinc (His, His, His, Asp) #status predicted

F:142/Active site: Arg #status predicted

Query Match 100.0%; Score 7; DB 2; Length 153;

Best Local Similarity 57.1%; Pred. No. 5.5e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

Db 28 VHVHAEP 34

RESULT 75

B64640

acyl carrier protein - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: B64640

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: B64640

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <TOM>

A:Cross-references: UNIPROT:O25615; GB:AE000605; GB:AE000511; NID:g2314103; PIDN:AAD080

C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology

C:Keywords: carrier protein

F:78-148/Domain: acyl carrier protein homology <ACP>

Query Match 100.0%; Score 7; DB 2; Length 153;

Best Local Similarity 57.1%; Pred. No. 5.5e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7

Db 99 VTPEAEP 105

RESULT 76

A69271

hypothetical protein AF0169 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: A69271

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F

.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: A69271

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <KLE>

A:Cross-references: UNIPROT:Q30068; GB:AE001094; GB:AE000782; NID:g2689417; PIDN:AAB910

C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF0169

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Query Match      100.0%; Score 7; DB 2; Length 153;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 68 VTKRAEF 74

RESULT 77
S77188
hypothetical protein slr1814 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S77188
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77188
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <KAN>
A;Cross-references: UNIPROT:P73699; EMBL:D90908; GB:AB001339; NID:gl652725; PIDN:BAA1774
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: hypothetical protein slr1203

Query Match      100.0%; Score 7; DB 2; Length 154;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 71 VYMQAEF 77

RESULT 78
S43227
homeotic protein PROX3 - Ephydatia fluviatilis (fragment)
C;Species: Ephydatia fluviatilis
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: S43227
R;Seimiya, M.; Ishiguro, H.; Miura, K.; Watanabe, Y.; Kurosawa, Y.
Eur. J. Biochem. 221, 219-225, 1994
A;Title: Homeobox-containing genes in the most primitive metazoa, the sponges.
A;Reference number: S43225; MUID:94222064; PMID:7909517
A;Accession: S43227
A;Molecule type: DNA
A;Residues: 1-157 <SEI>
A;Cross-references: UNIPROT:Q24785; GB:L23476; NID:g438584; PIDN:AAA20151.1; PID:g507133
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;16-74/Domain: homeobox homology <HOX>

Query Match      100.0%; Score 7; DB 2; Length 157;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 44 VAEAAEF 50

RESULT 79
B5658
18K protein GP18C - Lactococcus phage mi7-9
C;Species: Lactococcus phage mi7-9
A;Note: host Lactococcus lactis subsp. lactis
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-Jul-2000
C;Accession: B5658

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R;Kim, S.G.; Bor, Y.C.; Batt, C.A.
J. Dairy Sci. 75, 1761-1767, 1992
A;Title: Bacteriophage resistance in Lactococcus lactis ssp. lactis using antisense rib
A;Reference number: A5658; MUID:92364122; PMID:1500572
A;Accession: B5658
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-158 <KIM>
A;Cross-references: GB:S42434; NID:G253573; PIDN:AAB2891.1; PID:G253575
A;Experimental source: Lactococcus lactis subsp. lactis CC9
A;Note: sequence extracted from NCBI backbone (NCBIN:111067, NCBIPI:111071)
C;Superfamily: Streptococcus phage phi-O1205 hypothetical protein 11

Query Match      100.0%; Score 7; DB 2; Length 158;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 10 VQSHAEF 16

RESULT 80
C87486
hypothetical protein CC1912 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87486
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <STO>
A;Cross-references: UNIPROT:Q9A714; GB:AE005673; NID:gl3423365; PIDN:AAK23887.1; GSPDB:
C;Genetics:
C;Superfamily: (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase

Query Match      100.0%; Score 7; DB 2; Length 159;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 142 VAAAEAF 148

RESULT 81
E69531
molybdopterin-guanine dinucleotide biosynthesis protein B (mobB) homolog - Archaeoglobus
C;Species: Archaeoglobus fulgidus
C;Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: E69531
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69531
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-159 <KLE>
A;Cross-references: UNIPROT:O28031; GB:AE000949; GB:AE000782; NID:G2689272; PIDN:AA8990
C;Superfamily: Molybdenum cofactor guanine dinucleotide biosynthesis adapter protein Mo

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Query Match      100.0%; Score 7; DB 2; Length 159;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |:::|
Db 147 VERIAEF 153

RESULT 82
S00764
H+-transporting two-sector ATPase (EC 3.6.3.14) chain d - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00764
R:Walker, J.E.; Runswick, M.J.; Poulter, L.
J. Mol. Biol. 197, 89-100, 1987
A:Title: ATP synthase from bovine mitochondria: the characterization and sequence analysis
A:Reference number: S00763; MUID:88062745; PMID:2890767
A:Accession: S00764
A:Molecule type: mRNA
A:Residues: 1-161 <WAL>
A:Cross-references: UNIPROT:PI3620; EMBL:X06089; NID:g12791; PIDN:CAA29473.1; PID:g59987
C:Superfamily: H+-transporting ATP synthase chain d
C:Keywords: ATP biosynthesis; hydrolase; mitochondrion
F;2-161/Product: H+-transporting ATP synthase chain d #status predicted <MAT>

Query Match      100.0%; Score 7; DB 2; Length 161;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |:::|
Db 98 VKSCAEF 104

RESULT 83
D69439
conserved hypothetical protein AF1517 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69439
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69439
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <KLE>
A:Cross-references: UNIPROT:O28755; GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB8973
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1517

Query Match      100.0%; Score 7; DB 2; Length 162;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |:::|
Db 87 VGEAEF 93

RESULT 84
S60665
dihydrofolate reductase (EC 1.5.1.3) - Escherichia coli
C:Species: Escherichia coli
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S60665
R;Adrian, P.V.; Thomson, C.J.; Klugman, K.P.; Amyes, S.G.

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submitted to the EMBL Data Library, August 1995
A:Description: Nucleoside sequence of the cassette-borne type XIII dihydrofolate reduct.
A:Reference number: S60664
A:Accession: S60665
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <ADR>
A:Cross-references: UNIPROT:Q59408; EMBL:Z50802; NID:gl841698; PIDN:CAA90683.1; PID:g995
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology
C:Keywords: NADP; oxidoreductase
F;7-112/Domain: type I dihydrofolate reductase homology <DFR>

Query Match      100.0%; Score 7; DB 2; Length 165;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |:::|
Db 135 VLNAAEF 141

RESULT 85
S64794
hypothetical protein YLL042c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L0737
C:Species: Saccharomyces cerevisiae
C>Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: S64794
R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64794
A:Molecule type: DNA
A:Residues: 1-167 <WED>
A:Cross-references: UNIPROT:Q07879; EMBL:Z73147; NID:gl360236; PIDN:CAA97493.1; PID:g13
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:APG10; MIPS:YLL042c
A:Cross-references: SGD:S0003965
A:Map position: 12L
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLL042c

Query Match      100.0%; Score 7; DB 2; Length 167;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |:::|
Db 139 VGDQAEF 145

RESULT 86
A69422
hydrogenase maturation factor AF1378 [similarity] - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2003
C:Accession: A69422
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69422
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-168 <KLE>
A:Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AAB89866.1; PID:g26491
C:Superfamily: [Nife]-hydrogenase maturation protease

Query Match      100.0%; Score 7; DB 2; Length 168;

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Best Local Similarity 57.1%; Pred. No. 6e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXAAEF 7
Db 117 VKNLAEF 123

RESULT 87
AB0622
probable bacteriophage protein STY1051 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0622
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-168 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05444.1; PID:g16502205; GSPDB:GN00176
C;Genetics:
A;Gene: STY1051

Query Match 100.0%; Score 7; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 146 VLTNAEF 152

RESULT 88
HMECBM
M-agglutinin precursor - Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A27165
R;Rhen, M.; Vaisanen-Rhen, V.; Saraste, M.; Korhonen, T.K.
Gene 49, 351-360, 1986
A;Title: Organization of genes expressing the blood-group-M-specific hemagglutinin of Es
A;Reference number: A27165; MUID:87192025; PMID:2883087
A;Accession: A27165
A;Molecule type: DNA
A;Residues: 1-170 <RHE>
A;Cross-references: UNIPROT:P05818; GB:M15677; NID:G145437; PIDN:AAA23523.1; PID:g145438
C;Comment: This protein is a nonfimbrial hemagglutinin that is specific for blood group
C;Genetics:
A;Gene: bnaE
C;Superfamily: M-agglutinin
C;Keywords: hemagglutinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-170/Product: M-agglutinin #status predicted <MAT>

Query Match 100.0%; Score 7; DB 1; Length 170;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 33 VESDAEF 39

RESULT 89
T08348
hypothetical protein H1517 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100

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C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08348
R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: magaplasamid or
A;Reference number: Z16408; MUID:99063795; PMID:9847077
A;Accession: T08348
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-170 <DAS>
A;Cross-references: UNIPROT:O52035; EMBL:AF016485; NID:g2822278; PID:g2822409; HALOSP:B
A;Experimental source: strain NRC-1
C;Genetics:
A;Gene: HALOSP:H1517
A;Genome: plasmid pNRC100

Query Match 100.0%; Score 7; DB 2; Length 170;
Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 73 VDLDAEF 79

RESULT 90
A55629
19K Golgi apparatus protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55629; S49762
R;Saberan-Djoneidi, D.; Marey-Semper, I.; Picart, R.; Studler, J.M.; Tougaard, C.; Glow
J. Biol. Chem. 270, 1888-1893, 1995
A;Title: A 19-kDa protein belonging to a new family is expressed in the Golgi apparatus
A;Reference number: A55629; MUID:95130572; PMID:7829526
A;Accession: A55629
A;Molecule type: mRNA
A;Residues: 1-171 <SAB>
A;Cross-references: UNIPROT:P47759; GB:U17259; NID:g602139; PIDN:AAA67764.1; PID:g60214
C;Superfamily: brain neuron cytoplasmic protein 1
C;Keywords: Golgi apparatus

Query Match 100.0%; Score 7; DB 2; Length 171;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 64 VPKIAEF 70

RESULT 91
T37090
probable secreted protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37090
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21588
A;Accession: T37090
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-171 <SAU>
A;Cross-references: UNIPROT:Q9S1W6; EMBL:AL109950; PIDN:CAB52941.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ4.07

Query Match 100.0%; Score 7; DB 2; Length 171;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;

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Matches	4;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	VXXAAEF 7							
DB	91	VLSKAEF 97							
RESULT 92									
H95272									
hypothetical protein Sma0166 [imported] - Sinorhizobium meliloti (strain 1021) magaplasma									
C:Species: Sinorhizobium meliloti									
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004									
C:Accession: H95272									
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows									
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.									
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001									
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti									
A:Reference number: A95262; MUID:21396509; PMID:11481432									
A:Accession: H95272									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-176 <KUR>									
A:Cross-references: UNIPROT:Q930V6; GB:AE006469; PIDN:AAK64746.1; PID:G14523151; GSPDB:C									
A:Experimental source: strain 1021, megaplasmid pSymA									
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,									
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;									
L.; Hyman, R.W.; Jones, T.									
Science 293, 668-672, 2001									
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,									
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.									
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.									
A:Reference number: A96039; MUID:21368234; PMID:11474104									
A:Contents: annotation									
C:Genetics:									
A:Gene: Sma0166									
A:Genome: plasmid									
Query Match	100.0%;	Score 7;	DB 2;	Length 176;					
Best Local Similarity	57.1%;	Pred. No. 6.2e+02;							
Matches	4;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	VXXAAEF 7							
DB	43	VLSGAEF 49							
RESULT 93									
A72154									
E3L protein - variola minor virus (strain Garcia-1966)									
C:Species: variola minor virus									
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004									
C:Accession: A72154									
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopax									
submitted to GenBank, March 1998									
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor									
A:Reference number: A72150									
A:Accession: A72154									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-179 <SHC>									
A:Cross-references: UNIPROT:Q89086; GB:Y16780; NID:g5830555; PIDN:CAB54627.1; PID:e15425									
A:Experimental source: strain Garcia-1966									
C:Genetics:									
A:Gene: E3L									
Query Match	100.0%;	Score 7;	DB 2;	Length 179;					
Best Local Similarity	57.1%;	Pred. No. 6.3e+02;							
Matches	4;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	VXXAAEF 7							
DB	133	VGRNAEF 139							

RESULT 94									
T51128									
isopentenyl diphosphate isomerase [imported] - Brevibacterium linens									
C:Species: Brevibacterium linens									
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004									
C:Accession: T51128									
R:Krubasik, P.; Sandmann, G.									
Mol. Gen. Genet. 263, 423-432, 2000									
A:Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyc									
A:Reference number: Z25303; MUID:20279196; PMID:10821176									
A:Accession: T51128									
A:Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: DNA									
A:Residues: 1-182 <KRU>									
A:Cross-references: UNIPROT:Q9KK75; EMBL:AF139916; PIDN:AAF65591.1									
A:Experimental source: DSM 20426; ATCC9175									
C:Genetics:									
A:Gene: idi									
C:Superfamily: isopentenylidiphosphate isomerase									
Query Match	100.0%;	Score 7;	DB 2;	Length 182;					
Best Local Similarity	57.1%;	Pred. No. 6.4e+02;							
Matches	4;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	VXXAAEF 7							
DB	78	VSRRAEF 84							
RESULT 95									
C69133									
DNA-dependent RNA polymerase, subunit E' - Methanobacterium thermoautotrophicum (strain									
C:Species: Methanobacterium thermoautotrophicum									
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C:Accession: C69133									
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;									
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N									
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.									
J. Bacteriol. 179, 7135-7155, 1997									
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct									
A:Reference number: A69000; MUID:98037514; PMID:9371463									
A:Accession: C69133									
A:Status: preliminary; nucleic acid sequence not shown; translation not shown									
A:Molecule type: DNA									
A:Residues: 1-184 <MTH>									
A:Cross-references: UNIPROT:Q26364; GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AA8847,									
A:Experimental source: strain Delta H									
C:Genetics:									
A:Gene: MTH264									
A:Start codon: TTG									
C:Superfamily: DNA-directed RNA polymerase subunit E									
Query Match	100.0%;	Score 7;	DB 2;	Length 184;					
Best Local Similarity	57.1%;	Pred. No. 6.4e+02;							
Matches	4;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	VXXAAEF 7							
DB	89	VIEIAEF 95							
RESULT 96									
A12281									
nutrient-stress induced DNA binding protein [imported] - Nostoc sp. (strain PCC 7120)									
C:Species: Nostoc sp. PCC 7120									
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120									
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004									
C:Accession: A12281									
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;									
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, T									
DNA Res. 8, 205-213, 2001									
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana									

A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: A12281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <KUR>
A;Cross-references: UNIPROT:O8VQL3; GB:BA000019; PIDN:BA075507.1; PID:g17132942; GSPDB:G85763
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3808

Query Match 100.0%; Score 7; DB 2; Length 184;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|:|
DB 53 VVEGAEF 59

RESULT 97
T33039
hypothetical protein T22B2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33039
R;Bentley, D.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid T22B2.
A;Reference number: T21267
A;Accession: T33039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <BEN>
A;Cross-references: UNIPROT:O45194; EMBL:AF047662; PIDN:AAC04441.1; GSPDB:GN000028; CESP:
A;Experimental source: strain Bristol N2; clone T22B2
C;Genetics:
A;Gene: CESP:T22B2.2
A;Map position: X
A;Introns: 68/1; 95/2; 166/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T22B2.2

Query Match 100.0%; Score 7; DB 2; Length 185;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|:|
DB 83 VWSKAEF 89

RESULT 98
A39658
polyposis coli region hypothetical protein DP1 - human
N;Alternate names: deleted in polyposis 1 (DP1)
C;Species: Homo sapiens (man)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C;Accession: A39658
R;Joslyn, G.; Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grod-
arrington, J.; McPherson, J.; Wasmuth, J.; Le Faslier, D.; Abderrahim, H.; Cohen, D.; Le
Cell 66, 601-613, 1991
A;Title: Identification of deletion mutations and three new genes at the familial polypos-
is locus on chromosome 10p16.
A;Reference number: A39658; MUID:91330307; PMID:1678319
A;Accession: A39658
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <JOS>
A;Cross-references: UNIPROT:Q00765; GB:M73547; NID:g190161; PIDN:AAA60136.1; PID:g190162

Query Match 100.0%; Score 7; DB 2; Length 185;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

DB 91 VFSIAEF 97
|:|:|:|:|

RESULT 99
JC4667
TB2/DP1 protein homolog - mouse
N;Alternate names: deleted in polyposis protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4667
R;Prieschl, E.E.; Pendl, G.G.; Harner, N.E.; Baumruker, T.
Gene 169, 215-218, 1996
A;Title: The murine homolog of TB2/DP1, a gene of the familial adenomatous polyposis (FAP)
A;Reference number: JC4667; MUID:96194804; PMID:8647449
A;Accession: JC4667
A;Molecule type: mRNA
A;Residues: 1-185 <PRI>
A;Cross-references: UNIPROT:Q60870; GB:U28168; NID:g1142715; PIDN:AAB07994.1; PID:g1142
A;Experimental source: mast cell
C;Comment: This protein is one of the six proteins deleted in severe cases of familial
C;Genetics:
A;Gene: tb2/dpi
A;Map position: 5q21

Query Match 100.0%; Score 7; DB 2; Length 185;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|:|
DB 91 VFSIAEF 97

RESULT 100
AB0680
spermidine N1-acetyltransferase [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0680
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero-
var Typhi.
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0680
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01811.1; PID:g16502656; GSPDB:GN00176
C;Genetics:
A;Gene: STY1561
C;Superfamily: Escherichia coli ribosomal-protein-alanine N-acetyltransferase rimJ

Query Match 100.0%; Score 7; DB 2; Length 186;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|:|
DB 80 VHRRAEF 86

RESULT 101
G85763
spermidine N1-acetyltransferase [imported] - Escherichia coli (strain O157:H7, substrat-
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85763
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe-

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: G85763
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-186 <STO>
 A;Cross-references: UNIPROT:P37354; GB:AE005174; NID:G12515559; PIDN:AAG56571.1; GSPDB:C
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: speG
 C;Superfamily: *Escherichia coli* ribosomal-protein-alanine N-acetyltransferase rimJ

Query Match 100.0%; Score 7; DB 2; Length 186;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |::|||
 DB 80 VHHRAEF 86

RESULT 102
 A53345
 diamine N-acetyltransferase (EC 2.3.1.57) [validated] - *Escherichia coli* (strain K-12)
 N;Alternate names: spermidine acetyltransferase
 C;Species: *Escherichia coli*
 C;Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 09-Jul-2004
 C;Accession: A53345; B64914; T47116
 R;Fukuchi, J.; Kashiwagi, K.; Takio, K.; Igarashi, K.
 J. Biol. Chem. 269, 22581-22585, 1994
 A;Title: Properties and structure of spermidine acetyltransferase in *Escherichia coli*.
 A;Reference number: A55345; MUID:94357898; PMID:8077207
 A;Accession: A55345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-186 <FUK>
 A;Cross-references: UNIPROT:P37354; GB:D25276; NID:G517104; PIDN:BAA04966.1; PID:G517105
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: B64914
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-186 <BLAT>
 A;Cross-references: GB:AE000254; GB:U00096; NID:G1787862; PIDN:AACT4656.1; PID:G1787867;
 A;Experimental source: strain K-12, substrain MG1655
 R;Fukuchi, J.; Kashiwagi, K.; Yamagishi, M.; Ishihama, A.; Igarashi, K.
 J. Biol. Chem. 270, 18831-18835, 1995
 A;Title: Decrease in Cell Viability Due to the Accumulation of Spermidine in Spermidine
 A;Reference number: Z24355; MUID:95370188; PMID:7642535
 A;Accession: T47116
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-186 <FU2>
 A;Cross-references: EMBL:D25276; NID:G517104; PIDN:BAA04966.1; PID:G517105
 A;Experimental source: strain K-12; substrain W3110
 C;Genetics:
 A;Gene: speG
 C;Function:
 A;Description: EC 2.3.1.57 [validated, MUID:94357898], catalyzes the reversible reaction
 A;Note: alternative substrate spermine
 C;Superfamily: *Escherichia coli* ribosomal-protein-alanine N-acetyltransferase rimJ
 C;Keywords: acyltransferase; coenzyme A; homotetramer
 F;2-186/Product: diamine N-acetyltransferase #status experimental <MAT>

Query Match 100.0%; Score 7; DB 2; Length 186;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |::|||
 DB 80 VHHRAEF 86

RESULT 103
 B90915
 spermidine N1-acetyltransferase [imported] - *Escherichia coli* (strain O157:H7, substrain
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: B90915
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: B90915
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-186 <HAY>
 A;Cross-references: UNIPROT:P37354; GB:BA000007; PIDN:BA835713.1; PID:G13361756; GSPDB:C
 A;Experimental source: strain O157:H7, substrain RMD 0509952
 C;Genetics:
 A;Gene: BCS2290
 C;Superfamily: *Escherichia coli* ribosomal-protein-alanine N-acetyltransferase rimJ

Query Match 100.0%; Score 7; DB 2; Length 186;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |::|||
 DB 80 VHHRAEF 86

RESULT 104
 A86847
 acyltransferase [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
 C;Species: *Lactococcus lactis* subsp. *lactis*
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86847
 R;Dolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrh
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: A86847
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-187 <STO>
 A;Cross-references: UNIPROT:Q9CEQ9; GB:AE005176; PID:G12724800; PIDN:AAK05875.1; GSPDB:C
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: bar
 C;Superfamily: phosphinothricin N-acetyltransferase

Query Match 100.0%; Score 7; DB 2; Length 187;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
 |::|||
 DB 33 VPTIAEF 39

RESULT 105
 A83210
 probable deoxycytidine triphosphate deaminase PA3480 [imported] - *Pseudomonas aeruginos*
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: A83210
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bl
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.N.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <STO>
A;Cross-references: UNIPROT:Q9HVC9; GB:AE004769; GB:AE004091; NID:g9949624; PIDN:AAG0686
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3480
C;Superfamily: dCTP deaminase

Query Match 100.0%; Score 7; DB 2; Length 188;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 47 VRCAAEF 53

RESULT 106
F83290
translation elongation factor P PA2851 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83290
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bhardwaj, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83290
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <STO>
A;Cross-references: GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AAG06239.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: efp; PA2851
C;Superfamily: translation elongation factor EF-P

Query Match 100.0%; Score 7; DB 2; Length 188;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 21 VIQAAEF 27

RESULT 107
E84355
DNA-directed RNA polymerase subunit E' [imported] - *Halobacterium* sp. NRC-1
C;Species: *Halobacterium* sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84355
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, J.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, J.; Jung, K.H.; Alam, M.; Freitas, T.
A;Title: Genome sequence of *Halobacterium* species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <STO>
A;Cross-references: UNIPROT:Q9HNL1; GB:AE004437; NID:g10581476; PIDN:AAG20209.1; GSPDB:GN001
C;Genetics:
A;Gene: rpoE'

C;Superfamily: DNA-directed RNA polymerase subunit E

Query Match 100.0%; Score 7; DB 2; Length 190;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 66 VYEAEF 72

RESULT 108
S41476
calretinin - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S41476; S34391
R;Ellis, J.; Rogers, J.
Nucleic Acids Res. 21, 5171-5178, 1993
A;Title: Design and specificity of hammerhead ribozymes against calretinin mRNA.
A;Reference number: S41476; MUID:9407721; PMID:8255773
A;Accession: S41476
A;Molecule type: mRNA
A;Residues: 1-190 <ELL>
A;Cross-references: UNIPROT:Q08331; EMBL:X73985; NID:g393386; PIDN:CAA52163.1; PID:g393
C;Superfamily: calretinin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF hand
F;26-58/Domain: calmodulin repeat homology <EF3>
F;70-102/Domain: calmodulin repeat homology <EF4>
F;114-146/Domain: calmodulin repeat homology <EF5>

Query Match 100.0%; Score 7; DB 2; Length 190;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 25 VGSSAEF 31

RESULT 109
F84366
hypothetical protein Vng2162c [imported] - *Halobacterium* sp. NRC-1
C;Species: *Halobacterium* sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84366
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, J.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, J.; Jung, K.H.; Alam, M.; Freitas, T.
A;Title: Genome sequence of *Halobacterium* species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84366
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <STO>
A;Cross-references: UNIPROT:Q9HNC2; GB:AE004437; NID:g10581579; PIDN:AAG20298.1; GSPDB:GN001
C;Genetics:
A;Gene: VNG2162C

Query Match 100.0%; Score 7; DB 2; Length 190;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 180 VDAAEF 186

RESULT 110
T34819
hypothetical protein SC2E9.08 - *Streptomyces coelicolor*

C;Species: Streptomyces coelicolor
C;Date: 03-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34819
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21558
A;Accession: T34819
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-194 <OLI>
A;Cross-references: UNIPROT:O541133; EMBL:AL021530; PIDN:CAA16476.1; GSPDB:GN00070; SCOEED
A;Experimental source: strain A3(2)
C;Genetics:
C;Superfamily: Streptomyces coelicolor hypothetical protein SC2E9.08

Query Match 100.0%; Score 7; DB 2; Length 194;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|::|||
Db 58 VSITAEF 64

RESULT 111
E75496
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75496
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <WHI>
A;Cross-references: UNIPROT:Q9RWP2; GB:AE001920; GB:AE005013; NID:g6458318; PIDN:AAF1020
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0624
A;Map position: 1

Query Match 100.0%; Score 7; DB 2; Length 198;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|::|||
Db 123 VVGSAAEF 129

RESULT 112
F45456
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Paracoccus denitrificans
N;Alternate names: NADH-ubiquinone oxidoreductase chain 6
C;Species: Paracoccus denitrificans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: F45456
R;Xu, X.; Matsuno-Yagi, A.; Yagi, T.
Biochemistry 32, 968-981, 1993
A;Title: DNA sequencing of the seven remaining structural genes of the gene cluster encod
A;Reference number: A45456; MUID:93136200; PMID:8422400
A;Accession: F45456
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <XU1>
A;Cross-references: UNIPROT:P29922; GB:L02354; GB:L01096; NID:g150606; PIDN:AAA25596.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBI:P:123416)

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6
C;Keywords: membrane-associated complex; NAD; oxidoreductase; transmembrane protein

Query Match 100.0%; Score 7; DB 1; Length 200;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|::|||
Db 45 VLQGAEEF 51

RESULT 113
T02868
probable GTP-binding protein - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02868
R;foon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.
submitted to the EMBL Data Library, February 1998
A;Description: Molecular cloning and characterization of a cDNA encoding GTP-binding prot
A;Reference number: Z14741
A;Accession: T02868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-203 <YOO>
A;Cross-references: UNIPROT:O65038; EMBL:AF050675; NID:g2961177; PIDN:AAC05675.1; PID:g
A;Experimental source: strain Ilpoombyeo
C;Superfamily: ADP-ribosylation factor
C;Keywords: nucleotide binding; P-loop
F;24-31/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 7; DB 2; Length 203;
Best Local Similarity 57.1%; Pred. No. 7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|::|||
Db 12 VFSKAEF 18

RESULT 114
T41226
probable ser-thr protein kinase - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T41226
R;Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21979
A;Accession: T41226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-203 <LYN>
A;Cross-references: EMBL:AL035075; PIDN:CAA22632.1; GSPDB:GN00068; SPDB:SPCC1919.01
A;Experimental source: strain 972h-; cosmid c1919
C;Genetics:
A;Gene: SPDB:SPCC1919.01
A;Map position: 3

Query Match 100.0%; Score 7; DB 2; Length 203;
Best Local Similarity 57.1%; Pred. No. 7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|::|||
Db 118 VIAFAEF 124

RESULT 115
H75102
hypothetical protein PAB1577 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: H75102
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: H75102
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-203 <KAW>
 A;Cross-references: UNIPROT:Q9U2D4; GB:AJ248286; GB:AL096936; NID:G5458366; PIDN:CA85012
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1577

Query Match 100.0%; Score 7; DB 2; Length 203;
 Best Local Similarity 57.1%; Pred. No. 7e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 171 VGMIAEF 177

RESULT 116

H87489
 NADH dehydrogenase I, J subunit CCL1941 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: H87489
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heideberg, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: H87489
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-205 <SPO>
 A;Cross-references: UNIPROT:Q9A6Y5; GB:AE005673; NID:G13423398; PIDN:AAK23916.1; GSPDB:G

C;Genetics:
 A;Gene: CCL1941
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6

Query Match 100.0%; Score 7; DB 2; Length 205;
 Best Local Similarity 57.1%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 47 VLGAEF 53

RESULT 117

F72422
 2-dehydro-3-deoxy-phosphogluconate aldolase (EC 4.1.2.14) - Thermotoga maritima (strain N;Contains: 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14); 4-hydroxy-2-oxoglutarate: Thermotoga maritima
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: F72422
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: F72422
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-205 <ARN>
 A;Cross-references: UNIPROT:Q9WXS1; GB:AF001693; GB:AE000512; NID:G4980547; PIDN:AAD3516
 A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TW0066
 C;Superfamily: 2-dehydro-3-deoxyphosphogluconate aldolase
 C;Keywords: aldehyde-lyase; carbon-carbon lyase; oxo-acid-lyase
 F;40/Active site: Glu #status predicted
 F;129/Active site: Lys (covalent pyruvate-binding) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 205;
 Best Local Similarity 57.1%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 80 VESGAEF 86

RESULT 118

A97943
 hypothetical protein spr0569 [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C;Accession: A97943
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: A97943
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-206 <KUR>
 A;Cross-references: UNIPROT:Q8CZ19; GB:AE007317; PIDN:AAK99373.1; PID:G15458148; GSPDB:

C;Genetics:
 A;Gene: spr0569

Query Match 100.0%; Score 7; DB 2; Length 206;
 Best Local Similarity 57.1%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 81 VPIDAEF 87

RESULT 119

T19847
 hypothetical protein C39E9.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T19847
 R;Sims, M.

submitted to the EMBL Data Library, March 1996
 A;Reference number: Z19187
 A;Accession: T19847
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-209 <WIL>
 A;Cross-references: UNIPROT:Q18538; EMBL:Z70307; PIDN:CAA94330.1; GSPDB:GN00022; CESP:C
 A;Experimental source: clone C39E9
 C;Genetics:
 A;Gene: C39E9.4
 A;Map position: 4
 A;Introns: 14/1; 60/3; 177/2
 C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 100.0%; Score 7; DB 2; Length 209;
 Best Local Similarity 57.1%; Pred. No. 7.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 0;

Qy 1 VXXXXAEF 7
 |:::|

Db 14 VLVDAEF 20

RESULT 120

S26078
ribosomal protein S6, cytosolic - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 15-Sep-2003
C:Accession: S26078; S25550
R:Hansen, G.; Estruch, J.J.; Spena, A.
Nucleic Acids Res. 20, 5230, 1992
A:Title: Tobacco cDNA encoding the ribosomal protein S6.
A:Reference number: S26078; MUID:93027271; PMID:1408841
A:Accession: S26078
A:Molecule type: mRNA
A:Residues: 1-211 <HAN>
A:Cross-references: EMBL:X68050
R:Hansen, G.; Estruch, J.J.; Pisabarro, G.; Sommer, H.; Spena, A.
submitted to the EMBL Data Library, August 1992
A:Reference number: S25550
A:Accession: S25550
A:Molecule type: mRNA
A:Residues: 20-211 <HAN>
A:Cross-references: EMBL:X68050; NID:g20021; PIDN:CAA48187.1; PID:g20022
C:Superfamily: ribosomal protein S6, eukaryotic type
C:Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 100.0%; Score 7; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. No. 7.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||

Db 124 VNTAAEF 130

RESULT 121

I50543
aryl hydrocarbon receptor - mummichog (fragment)
C:Species: Fundulus heteroclitus (mummichog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50543
R:Hahn, M.E.; Karchner, S.I.
Biochem. J. 310, 383-387, 1995
A:Title: Evolutionary conservation of the vertebrate Ah (dioxin) receptor: amplification
A:Reference number: I50543; MUID:95382748; PMID:7654172
A:Accession: I50543
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-212 <HAH>
A:Cross-references: UNIPROT:Q90505; EMBL:U29679; NID:g976397; PID:g976398
C:Genetics:
A:Gene: AHR2

Query Match 100.0%; Score 7; DB 2; Length 212;
Best Local Similarity 57.1%; Pred. No. 7.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||

Db 58 VASDAEF 64

RESULT 122

T37237
H+-exporting ATPase (EC 3.6.3.6), vacuolar VHA-4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37237; T24332
R:Oka, T.; Yamamoto, R.; Futai, M.
J. Biol. Chem. 272, 24387-24392, 1997
A:Title: Three vha genes encode proteolipids of Caenorhabditis elegans vacuolar-type ATP
A:Reference number: Z21636; MUID:97450964; PMID:9305897

A:Accession: T37237
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-214 <OKA>
A:Cross-references: UNIPROT:Q22087; EMBL:AB000919; NID:g2467305; PIDN:BAA22597.1; PID:g2467305
R:Burton, J.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19876
A:Accession: T24332
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-214 <WIL>
A:Cross-references: EMBL:Z68137; PIDN:CAA92686.1; GSPDB:GN00020; CESP:T01H3.1
A:Experimental source: clone T01H3
C:Genetics:
A:Gene: VHA-4; T01H3.1
A:Map position: 2
A:Introns: 25/1; 69/2; 118/3
C:Superfamily: vacuolar H⁺-transporting ATPase 16K chain
C:Keywords: hydrolase; membrane-associated complex; transmembrane protein

Query Match 100.0%; Score 7; DB 2; Length 214;
Best Local Similarity 57.1%; Pred. No. 7.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||

Db 114 VGKLAEF 120

RESULT 123

H69251
hypothetical protein AF0016 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69251
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woesle, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeobacterium Pyrococcus furiosus
A:Reference number: A92550; MUID:98049343; PMID:9389475
A:Accession: H69251
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-215 <KLE>
A:Cross-references: UNIPROT:Q30219; GB:AE001105; GB:AE000782; NID:g2689428; PIDN:AAB9121

Query Match 100.0%; Score 7; DB 2; Length 215;
Best Local Similarity 57.1%; Pred. No. 7.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||

Db 196 VLRAAEF 202

RESULT 124

E97240
transcription regulators, AcrR family [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97240
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97240
A:Status: preliminary
A:Molecule type: DNA

```

A;Residues: 1-216 <KUR>
A;Cross-references: UNIPROT:Q97FHI; GB:AE001437; PIDN:AAK80712.1; PID:g15025805; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2768

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 216;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 39 VAKAAEF 45

RESULT 125
A24651
Chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Proteus mirabilis (strain PM13)
C;Species: Proteus mirabilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A24651
R;Charles, I.G.; Keyte, J.W.; Shaw, W.V.
J. Bacteriol. 164, 123-129, 1985
A;Title: Nucleotide sequence analysis of the cat gene of Proteus mirabilis: comparison w
A;Reference number: A24651; MUID:86008040; PMID:3900035
A;Accession: A24651
A;Molecule type: DNA
A;Residues: 1-217 <CHA>
A;Cross-references: UNIPROT:P07641; GB:M11587; NID:g150882; PIDN:AAA25655.1; PID:g150883
C;Genetics:
A;Gene: cat
C;Superfamily: chloramphenicol acetyltransferase
C;Keywords: acyltransferase; antibiotic resistance; coenzyme A; homotrimer

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 217;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 67 VNKAAEF 73

RESULT 126
G69092
Conserved hypothetical protein MTH1689 - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69092
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69092
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-217 <MTH>
A;Cross-references: UNIPROT:O27724; GB:AE000926; GB:AE000666; NID:g2622806; PIDN:AAB8616
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1689

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 217;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 107 VAPPAEF 113

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RESULT 127
A71879
Hypothetical protein jhp0866 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71879
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: A71879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <ARN>
A;Cross-references: UNIPROT:Q92K89; GB:AE001516; GB:AE001439; NID:g4155431; PIDN:AA064
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0866

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 219;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 77 VFTQAEF 83

RESULT 128
T19468
Hypothetical protein C25G4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19468
R;Percy, C.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z19127
A;Accession: T19468
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-221 <WIL>
A;Cross-references: UNIPROT:Q18169; EMBL:Z70680; PIDN:CAA94571.1; GSPDB:GN00022; CESP:
A;Experimental source: clone C25G4
C;Genetics:
A;Gene: CESP:C25G4.2
A;Map position: 4
A;Introns: 53/1; 118/3
C;Superfamily: hypothetical protein YMR222c

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 221;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 33 VKSLAEF 39

RESULT 129
C82498
ribosomal large chain pseudouridine synthase A VCA0104 [imported] - Vibrio cholerae (st
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82498
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82498

```

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <HE1>
A;Cross-references: UNIPROT:Q9KN61; GB:AE004353; GB:AE003853; NID:g9657488; PIDN:AAF9601
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
A;Gene: VCA0104
A;Map position: 2

Query Match 100.0%; Score 7; DB 2; Length 221;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 30 VNKPAEF 36

RESULT 130
E64205
deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: E64205
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64205
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-223 <TIGR>
A;Cross-references: UNIPROT:P47296; GB:U39684; GB:L43967; NID:G3844650; PIDN:AAC71266.1;
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Superfamily: deoxyribose-phosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 100.0%; Score 7; DB 2; Length 223;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 93 VNNIAEF 99

RESULT 131
H70529
hypothetical protein Rv2693c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70529
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70529
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-223 <COL>
A;Cross-references: UNIPROT:O07195; GB:Z96072; GB:AL123456; NID:G3261793; PIDN:CAB09483.
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv2693c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2693c

Query Match 100.0%; Score 7; DB 2; Length 223;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 210 VGGAAEF 216

RESULT 132
S02216
deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma pneumoniae
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C;Accession: S02216; S73417
R;Loechel, S.; Inamine, J.M.; Hu, P.C.
Nucleic Acids Res. 17, 801, 1989
A;Title: Nucleotide sequence of the deoC gene of Mycoplasma pneumoniae.
A;Reference number: S02216; MUID:89128453; PMID:2492658
A;Accession: S02216
A;Molecule type: DNA
A;Residues: 1-224 <LOE>
A;Cross-references: UNIPROT:P09924; EMBL:X13544; NID:G44480; PIDN:CAA31897.1; PID:G44481
R;Himmelreich, R.; Hilbert, H.; Plegens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73417
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-224 <HIM>
A;Cross-references: EMBL:AE000011; GB:U00089; NID:G1673740; PIDN:AAB95739.1; PID:G167374
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: deoC
A;Genetic code: SGC3
A;Superfamily: deoxyribose-phosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 100.0%; Score 7; DB 2; Length 224;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 93 VNNIAEF 99

RESULT 133
AH1187
hypothetical protein lmo0904 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1187
R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <GLA>
A;Cross-references: UNIPROT:Q8Y8J7; GB:NC_003210; PIDN:CAC98982.1; PID:G16410307; GSPDB
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0904

Query Match 100.0%; Score 7; DB 2; Length 224;

Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|:|
Db 157 VPLVAEF 163

RESULT 134
T17795
hypothetical protein A298L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17795
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17795
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-225 <GRA>
A;Cross-references: UNIPROT:Q84614; EMBL:U42580; NID:94028896; PIDN:AAC96666.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A298L

Query Match 100.0%; Score 7; DB 2; Length 225;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|:|
Db 9 VNMLAEF 15

RESULT 135
AG2327
deoxyribose-phosphate aldolase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2327
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2327
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <KUR>
A;Cross-references: UNIPROT:Q8YPM0; GB:BA000019; PIDN:BAB75873.1; PID:gl7133309; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4174
C;Superfamily: deoxyribose-phosphate aldolase

Query Match 100.0%; Score 7; DB 2; Length 226;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|:|
Db 50 VKQAAEF 56

RESULT 136
A53273
MHC class II histocompatibility antigen DR alpha chain - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A53273
R;Albright, D.; Bailey, E.; Woodward, J.G.

Immunogenetics 34, 136-138, 1991
A;Title: Nucleotide sequence of a cDNA clone of the horse (Equus caballus) DRA gene.
A;Reference number: A53273; MUID:91331619; PMID:1869308
A;Accession: A53273
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-226 <ALB>
A;Cross-references: UNIPROT:Q30489; GB:M60100; NID:gl64236; PIDN:AAA30956.1; PID:gl6423
C;Genetics:
A;Gene: DRA
A;Map position: 20
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;97-162/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 7; DB 2; Length 226;
Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|:|
Db 3 VIIQAEF 9

RESULT 137
T33591
hypothetical protein C40A11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33591
R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40A11.
A;Reference number: Z21374
A;Accession: T33591
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-227 <WAG>
A;Cross-references: UNIPROT:Q9TZA7; EMBL:AF099914; PIDN:AAC68760.1; GSPDB:GN000020; CESP
A;Experimental source: strain Bristol N2; clone C40A11
C;Genetics:
A;Gene: CESP:C40A11.2
A;Map position: 2
A;Introns: 40/3; 123/3; 161/1; 213/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 100.0%; Score 7; DB 2; Length 227;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:|:|:|:|
Db 83 VRREAEF 89

RESULT 138
S65425
pyruvate decarboxylase (EC 4.1.1.1) (clone PDC3) - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 12-Jul-2004
C;Accession: S65425
R;Muecke, U.; Wohlfarth, T.; Fiedler, U.; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S.
Eur. J. Biochem. 237, 373-382, 1996
A;Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino ac
A;Reference number: S65423; MUID:96215432; PMID:8647075
A;Accession: S65425
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-228 <WUE>
A;Cross-references: UNIPROT:Q7M227
C;Superfamily: thiamin pyrophosphate-binding domain homology
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 100.0%; Score 7; DB 2; Length 228;

```

Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 41 VEAAAEF 47

RESULT 139
S65426
pyruvate decarboxylase (EC 4.1.1.1) - fava bean (fragment)
C:Species: Vicia faba (fava bean)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 12-Jul-2004
C:Accession: S65426
R:Muecke, U.; Wohlfarth, T.; Fiedler, U.; Baumelein, H.; Ruecknagel, K.P.; Koenig, S.
Eur. J. Biochem. 237, 373-382, 1996
A:Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino acid
A:Reference number: S65423; MUID:96215432; PMID:8647075
A:Accession: S65426
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <MUE>
A:Cross-references: UNIPROT:Q7M228
C:Superfamily: thiamin pyrophosphate-binding domain homology
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 100.0%; Score 7; DB 2; Length 228;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 41 VEAAAEF 47

RESULT 140
AI2486
hypothetical protein alr7073 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AI2486
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakaaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <KUR>
A:Cross-references: UNIPROT:Q8YL62; GB:BA000020; PIDN:BA078157.1; PID:gl7135611; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7073
A:Genome: Plasmid

Query Match 100.0%; Score 7; DB 2; Length 228;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 26 VEAAAEF 32

RESULT 141
A48381
MHC class II histocompatibility antigen alpha chain - sheep
C:Species: Ovis sp. (sheep)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A48381
R:Ballingall, K.T.; Wright, H.; Redmond, J.; Dutia, B.M.; Hopkins, J.; Lang, J.; Deversid

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Anim. Genet. 23, 347-359, 1992
A:Title: Expression and characterization of ovine major histocompatibility complex class
A:Reference number: A48381; MUID:92367958; PMID:1503274
A:Accession: A48381
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-229 <BAL>
A:Experimental source: Suffolk
A:Note: sequence extracted from NCBI backbone (NCBIN:110906, NCBIN:110908, NCBI:110909)
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:100-165/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 7; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 6 VIIQAEF 12

RESULT 142
F87572
conserved hypothetical protein CC2609 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87572
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: F87572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <STO>
A:Cross-references: UNIPROT:Q9A555; GB:AE005673; NID:gl3424182; PIDN:AAK24578.1; GSPDB:G
C:Genetics:
A:Gene: CC2609

Query Match 100.0%; Score 7; DB 2; Length 230;
Best Local Similarity 57.1%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 213 VEIEAEF 219

RESULT 143
S37778
filamin, muscle - human (fragment)
N:Alternate names: actin-binding protein 280 homolog
C:Species: Homo sapiens (man)
C>Date: 07-Oct-1994 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S37778
R:Maestrini, E.; Patrosso, C.; Mancini, M.; Rivella, S.; Rocchi, M.; Repetto, M.; Villa,
Hum. Mol. Genet. 2, 761-766, 1993
A:Title: Mapping of two genes encoding isoforms of the actin binding protein ABP-280, a
A:Reference number: S37775; MUID:93357748; PMID:7689010
A:Accession: S37778
A:Molecule type: mRNA
A:Residues: 1-231 <MAE>
A:Cross-references: UNIPROT:Q14315; EMBL:X70083; NID:g312405; PIDN:CAA49688.1; PID:g9382
A:Note: S37775 may be a second fragment of the same protein
C:Genetics:
A:Map position: 7
C:Keywords: actin binding; cytoskeleton

Query Match 100.0%; Score 7; DB 2; Length 231;
Best Local Similarity 57.1%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VXXAAEF 7
      |:::|
Db      100 VDKPAEF 106

RESULT 144
T03329
probable amidase lytA - Lactococcus phage b1L170
N/Alternate names: gene 122 protein
C/Species: Lactococcus phage b1L170
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03329
R/Crutz-Le Coq, A.M.; Cesselin, B.; Comissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M
submitted to the EMBL Data Library, June 1997
A/Description: Sequence and organization of the lactococcal isometric b1L170 phage genom
A/Reference number: Z14903
A/Accession: T03329
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-233 <CRU>
A/Cross-references: UNIPROT:O80122; EMBL:AF009630; NID:g3282260; PIDN:AAC27201.1; PID:g3
C/Genetics:
A/Gene: 122

      Query Match      100.0%; Score 7; DB 2; Length 233;
      Best Local Similarity 57.1%; Pred. No. 7.8e+02;
      Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |:::|
Db      220 VELDPAEF 226

RESULT 145
S23401
chloride channel protein - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S23401; S36084
R/Faulmichl, M.; Li, Y.; Wickman, K.; Ackerman, M.; Peralta, E.; Clapham, D.
Nature 356, 238-241, 1992
A/Title: New mammalian chloride channel identified by expression cloning.
A/Reference number: S23401; MUID:92204230; PMID:1313151
A/Accession: S23401
A/Molecule type: mRNA
A/Residues: 1-235 <PAU>
A/Cross-references: UNIPROT:P35521; EMBL:X65450
A/Note: the authors translated the codon AAA for residue 85 as Leu
R/Peralta, E.
submitted to the EMBL Data Library, April 1992
A/Reference number: S36084
A/Accession: S36084
A/Molecule type: mRNA
A/Residues: 1-80, 'M', 82-235 <PER>
A/Cross-references: EMBL:X65450; NID:g839; PIDN:CAA46447.1; PID:g840
C/Genetics:
A/Gene: IC1n
C/Keywords: chloride channel; ion channel; transmembrane protein
F/30-40/Domain: transmembrane beta strand #status predicted <TM1>
F/49-59/Domain: transmembrane beta strand #status predicted <TM2>
F/49-53/Region: nucleotide binding #status predicted
F/60-68/Domain: transmembrane beta strand #status predicted <TM3>
F/77-88/Domain: transmembrane beta strand #status predicted <TM4>

      Query Match      100.0%; Score 7; DB 2; Length 235;
      Best Local Similarity 57.1%; Pred. No. 7.9e+02;
      Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |:::|
Db      104 VEPIAEF 110
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RESULT 146
B70728
hypothetical protein Rv2558 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: B70728
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: B70728
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <COL>
A/Cross-references: UNIPROT:Q50740; GB:Z77250; GB:AL123456; NID:g3261617; PIDN:CAB01046
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV2558

      Query Match      100.0%; Score 7; DB 2; Length 236;
      Best Local Similarity 57.1%; Pred. No. 7.9e+02;
      Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |:::|
Db      217 VLDVAEF 223

RESULT 147
D64855
probable transcription regulator ycfQ - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: D64855
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <BLAT>
A/Cross-references: GB:AE000211; GB:U00096; NID:gl787345; PIDN:AAC74195.1; PID:gl787354
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: ycfQ
C/Keywords: DNA binding; transcription regulation
F/67-86/Region: helix-turn-helix motif

      Query Match      100.0%; Score 7; DB 2; Length 236;
      Best Local Similarity 57.1%; Pred. No. 7.9e+02;
      Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |:::|
Db      193 VTHLAEF 199

RESULT 148
A90815
hypothetical protein ECs1489 [imported] - Escherichia coli (strain O157:H7, substrain R
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A90815
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
```

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A90815

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-236 <HAY>

A;Cross-references: UNIPROT:Q8X8G3; GB:BA000007; PIDN:BA034912.1; PID:gl33360953; GSPDB:G

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: ECs1489

Query Match 100.0%; Score 7; DB 2; Length 236;

Best Local Similarity 57.1%; Pred. No. 7.9e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

|:::|

Db 193 VTHLAEF 199

RESULT 149

E85674

hypothetical protein ycfQ [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: E85674

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E85674

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-236 <STO>

A;Cross-references: UNIPROT:Q8X8G3; GB:AE005174; NID:gl2514658; PIDN:AAG55857.1; GSPDB:G

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: ycfQ

Query Match 100.0%; Score 7; DB 2; Length 236;

Best Local Similarity 57.1%; Pred. No. 7.9e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

|:::|

Db 193 VTHLAEF 199

RESULT 150

D82318

conserved hypothetical protein VC0483 [imported] - Vibrio cholerae (strain N16961 serogr

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: D82318

R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82318

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-238 <HEI>

A;Cross-references: UNIPROT:Q9KUN2; GB:AE004134; GB:AE003852; NID:g9654900; PIDN:AAF9365

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0483

A;Map position: 1

Query Match 100.0%; Score 7; DB 2; Length 238;

Best Local Similarity 57.1%; Pred. No. 8e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

|:::|

Db 46 VPDMAEF 52

RESULT 151

F75035

iron (iii) abc transporter, ATP-binding protein (hemv-2) PAB1536 - Pyrococcus abyssi (s

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004

C;Accession: F75035

R;Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: F75035

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-238 <KAW>

A;Cross-references: UNIPROT:Q9UZ80; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB501.

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB1536

C;Superfamily: ATP-binding cassette homology

F;18-201/Domain: ATP-binding cassette homology <ABC>

Query Match 100.0%; Score 7; DB 2; Length 238;

Best Local Similarity 57.1%; Pred. No. 8e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

|:::|

Db 17 VLKNAEF 23

RESULT 152

AG0605

oxygen-insensitive NADPH nitroreductase (EC 1.-.-.-) [imported] - Salmonella enterica ser

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AG0605

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

. S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0605

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-240 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD05313.1; PID:gl6502077; GSPDB:GN00176

C;Genetics:

A;Gene: nfsA

C;Superfamily: NADPH-flavin oxidoreductase homolog

C;Keywords: oxidoreductase

Query Match 100.0%; Score 7; DB 2; Length 240;

Best Local Similarity 57.1%; Pred. No. 8e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

|:::|

Db 70 VAQAAEF 76

RESULT 153

I80318

drug activity modulator A - Escherichia coli (strain K-12)

N;Contains: aromatic nitrate reductase (NADPH) (EC 1.6.6.-) oxygen-insensitive

C;Species: Escherichia coli
 C;Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: I80318; C64823; S04774
 R;Chatterjee, P.K.; Sternberg, N.L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 8950-8954, 1995
 A;Title: A general genetic approach in Escherichia coli for determining the mechanism(s)
 A;Reference number: I59418; MUID:96004656; PMID:7568050
 A;Accession: I80318
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-240 <RES>
 A;Cross-references: UNIPROT:P17117; EMBL:U18655; NID:G609323; PIDN:AAC34350.1; PID:G6093
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: C64823
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-240 <BLAT>
 A;Cross-references: GB:AE000187; GB:U00096; NID:gl787070; PIDN:AAC73938.1; PID:gl787075;
 R;Experimental source: strain K-12, substrain MG1655
 R;Kang, W.K.; Icho, T.; Isono, S.; Kitakawa, M.; Isono, K.
 Mol. Gen. Genet. 217, 281-288, 1989
 A;Title: Characterization of the gene rimK responsible for the addition of glutamic acid
 A;Reference number: S04774; MUID:89364710; PMID:2570347
 A;Accession: S04774
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 134-154, 'CA', 157, 'AGH', 161-186, 'RHWRSMTSNWRNITSPVAALIGIPGAIISAEOQLKKAHLFWI
 A;Cross-references: GB:X15859; NID:G42745; PIDN:CAA33867.1; PID:G42746
 C;Genetics:
 A;Gene: mdA; mdA18
 A;Map position: 18.7-19.0 min
 C;Superfamily: NADPH-flavin oxidoreductase homolog
 C;Keywords: flavoprotein; FMN; oxidoreductase

Query Match 100.0%; Score 7; DB 2; Length 240;
 Best Local Similarity 57.1%; Pred. No. 8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 70 VAQAAEF 76

Db

RESULT 154
 C90745
 modulator of drug activity A [imported] - Escherichia coli (strain O157:H7, substrain R
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: C90745
 R;Hayaishi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: C90745
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-240 <HAY>
 A;Cross-references: UNIPROT:Q8X6S1; GB:BA000007; PIDN:BA834354.1; PID:gl3360390; GSPDB:C
 A;Experimental source: strain O157:H7, substrain RMD 0509952
 C;Genetics:
 A;Gene: EC80931
 C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 100.0%; Score 7; DB 2; Length 240;
 Best Local Similarity 57.1%; Pred. No. 8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 70 VAQAAEF 76

Db

RESULT 155
 G85595
 modulator of drug activity A [imported] - Escherichia coli (strain O157:H7, substrain E
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G85595
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: G85595
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-240 <STO>
 A;Cross-references: UNIPROT:Q8X6S1; GB:AE005174; NID:gl2513866; PIDN:AAG55227.1; GSPDB:
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: mdAa
 C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 100.0%; Score 7; DB 2; Length 240;
 Best Local Similarity 57.1%; Pred. No. 8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 70 VAQAAEF 76

Db

RESULT 156
 D82288
 NADPH-flavin oxidoreductase VC0715 [imported] - Vibrio cholerae (strain N16961 serogrou
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82288
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
 Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers,
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: D82288
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-240 <HEI>
 A;Cross-references: UNIPROT:Q9KU15; GB:AE004159; GB:AE003852; NID:9655156; PIDN:AAF938
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC0715
 A;Map position: 1
 C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 100.0%; Score 7; DB 2; Length 240;
 Best Local Similarity 57.1%; Pred. No. 8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 70 VASAAEF 76

Db

RESULT 157
 H64373
 hypothetical protein MJ0592 - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: H64373
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

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; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64373
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-240 <BL>
A:Cross-references: UNIPROT:Q80111; GB:U67508; GB:L77117; NID:g1591300; PIDN:AAB98586.1;
C:Genetics:
A:Map position: FOR525640-526362
A:Start codon: GTG

Query Match 100.0%; Score 7; DB 2; Length 240;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 173 VKIPAEF 179

RESULT 158
S23099
lectin I, anti-H(O) - Cytisus sessilifolius
C:Species: Cytisus sessilifolius
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S23099; S13438
R:Konami, Y.; Yamamoto, K.; Osawa, T.; Irimura, T.
FEBS Lett. 304, 129-135, 1992
A:Title: Correlation between carbohydrate-binding specificity and amino acid sequence of
A:Reference number: S23099; MUID:92316214; PMID:1618311
A:Accession: S23099
A:Molecule type: protein
A:Residues: 1-244 <KON>
A:Cross-references: UNIPROT:P22970
A:Experimental source: seed
R:Konami, Y.; Yamamoto, K.; Osawa, T.
Biol. Chem. Hoppe-Seyler 372, 103-111, 1991
A:Title: Purification and characterization of two types of Cytisus sessilifolius anti-H
A:Reference number: S13438; MUID:91315748; PMID:1859626
A:Accession: S13438
A:Molecule type: protein
A:Residues: 1-3,'K',5-23,'A',25-29,'K',31-35 <BIO>
A:Experimental source: seed
C:Superfamily: plant lectin
C:Keywords: calcium binding; glycoprotein; homotetramer; lectin; manganese; seed
F;116-129/Domain: Glycopeptide #status predicted <GLP>
F;113,117/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;127,129,140,145/Binding site: manganese (Glu, Asp, His) #status predicted
F;129,140/Binding site: calcium (Asp) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. No. 8.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 219 VGNAAEF 225

RESULT 159
T00825
probable heat shock transcription factor At2g41690 [imported] - Arabidopsis thaliana
N:Alternate names: heat shock transcription factor homolog T32G6.21
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00825; H64844
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.

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A:Reference number: Z14163
A:Accession: T00825
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-244 <ROU>
A:Cross-references: UNIPROT:Q22230; EMBL:AC002510; NID:g2618683; PID:g2618703
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <STO>
A:Cross-references: GB:AE002093; NID:g2618703; PIDN:AAB84350.1; GSPDB:GN00139
C:Genetics:
A:Gene: T32G6.21; At2g41690
A:Map position: 2
A:Introns: 99/3
F;41-136/Domain: HSF DNA-binding domain homology <HSF>

Query Match 100.0%; Score 7; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. No. 8.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 69 VWQPAEF 75

RESULT 160
H97182
uncharacterized conserved protein, YebC family CAC2295 [imported] - Clostridium acetobu
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97182
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 193, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97182
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <KUR>
A:Cross-references: UNIPROT:Q97GS1; GB:AE001437; PIDN:AAK80251.1; PID:g15025300; GSPDB:
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2295
C:Superfamily: hypothetical protein MG332

Query Match 100.0%; Score 7; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
Db 234 VYHNAEF 240

RESULT 161
T44353
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44353
R:Matsumita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 191, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A:Reference number: Z22752; MUID:99121032; PMID:9922257

```

A;Accession: T44353
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-246 <MAT>
 A;Cross-references: UNIPROT:Q9ZKNO; EMBL:AB014075; NID:G3868863; PIDN:BAA34259.1; PID:G3868863
 A;Experimental source: strain JCM 1403
 C;Superfamily: hypothetical protein MG332

Query Match 100.0%; Score 7; DB 2; Length 246;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 234 VYHNAEF 240

RESULT 162

S20940
 DNA-binding protein - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 22-Nov-1993 #sequence_revision 19-Jan-1996 #text_change 16-Aug-2004
 C;Accession: S20940; S59602
 R;Didier, D.K.; Klee, H.J.
 Plant Mol. Biol. 18, 977-979, 1992
 A;Title: Identification of an Arabidopsis DNA-binding protein with homology to nucleolin
 A;Reference number: S20940; MUID:92256819; PMID:1341899

A;Accession: S20940

A;Molecule type: mRNA

A;Residues: 5-246 <DID>

A;Cross-references: UNIPROT:Q39209; EMBL:X63157

A;Experimental source: FMV3bp

A;Accession: S59602

A;Molecule type: DNA

A;Residues: 1-4 <DIW>

A;Cross-references: EMBL:X63157

C;Superfamily: ribonucleoprotein repeat homology

F;68-135/Domain: ribonucleoprotein repeat homology <RRM1>

F;162-229/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 100.0%; Score 7; DB 2; Length 246;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 54 VSRAEF 60

RESULT 163

PQ0662
 outer capsid spike protein VP4 - feline rotavirus A (strain Cat2) (fragment)
 N;Alternate names: VP8* protein
 C;Species: feline rotavirus A
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0662
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A

A;Reference number: PQ0651; MUID:93346985; PMID:8393919

A;Accession: PQ0662

A;Molecule type: mRNA

A;Residues: 1-247 <NAK>

A;Cross-references: GB:D14621; NID:G287424; PIDN:BAA03472.1; PID:G287425

C;Comment: This protein plays a role in viral neutralization, viral virulence and haemagglutinin

C;Genetics:

A;Gene: VP4

C;Superfamily: rotavirus outer layer protein VP3

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 164

PQ0652
 outer capsid spike protein VP4 - human rotavirus (strain AU228) (fragment)
 N;Alternate names: VP8* protein
 C;Species: human rotavirus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0652
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the

A;Reference number: PQ0651; MUID:93346985; PMID:8393919

A;Accession: PQ0652

A;Molecule type: mRNA

A;Residues: 1-247 <NAK>

A;Cross-references: GB:D14615; NID:G287412; PIDN:BAA03466.1; PID:G287413

C;Comment: This protein plays a role in viral neutralization, viral virulence and haemagglutinin

C;Genetics:

A;Gene: VP4

C;Superfamily: rotavirus outer layer protein VP3

C;Keywords: hemagglutinin; outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 165

PQ0661
 outer capsid spike protein VP4 - human rotavirus (strain M258) (fragment)
 C;Species: human rotavirus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0661
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the

A;Reference number: PQ0651; MUID:93346985; PMID:8393919

A;Accession: PQ0661

A;Molecule type: mRNA

A;Residues: 1-247 <NAK>

A;Cross-references: GB:D14622; NID:G287426; PIDN:BAA03473.1; PID:G287427

C;Comment: This protein plays a role in viral neutralization, viral virulence and haemagglutinin

C;Genetics:

A;Gene: VP4

C;Superfamily: rotavirus outer layer protein VP3

C;Keywords: hemagglutinin; outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 166

PQ0655
 outer capsid spike protein VP4 - human rotavirus (strain AU379) (fragment)
 N;Alternate names: VP8* protein
 C;Species: human rotavirus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0655
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993

```

A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
A;Reference number: PQ0651; MUID:93346985; PMID:8393919
A;Accession: PQ0655
A;Molecule type: mRNA
A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14616; NID:g287414; PIDN:BAA03467.1; PID:g287415
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
A;Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein

Query Match      100.0%; Score 7; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
    |:::|
Db 199 VSSDAEF 205

RESULT 169
PQ0660
outer capsid spike protein VP4 - human rotavirus (strain PCP5) (fragment)
N;Alternate names: VP8* protein
C;Species: human rotavirus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0660
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the
A;Reference number: PQ0651; MUID:93346985; PMID:8393919
A;Accession: PQ0660
A;Molecule type: mRNA
A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14624; NID:g287430; PIDN:BAA03475.1; PID:g287431
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
A;Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein

Query Match      100.0%; Score 7; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
    |:::|
Db 199 VSSDAEF 205

RESULT 170
PQ0659
outer capsid spike protein VP4 - human rotavirus (strain PA151) (fragment)
N;Alternate names: VP8* protein
C;Species: human rotavirus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0659
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the
A;Reference number: PQ0651; MUID:93346985; PMID:8393919
A;Accession: PQ0659
A;Molecule type: mRNA
A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14623; NID:g287428; PIDN:BAA03474.1; PID:g287429
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
A;Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein

Query Match      100.0%; Score 7; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
    |:::|
Db 199 VSSDAEF 205

RESULT 171
PQ0658
outer capsid spike protein VP4 - human rotavirus (strain AU938) (fragment)
N;Alternate names: VP8* protein

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C;Species: human rotavirus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0658
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
 A;Reference number: PQ0651; MUID:93346985; PMID:8393919
 A;Accession: PQ0658
 A;Molecule type: mRNA
 A;Residues: 1-247 <NAK>
 A;Cross-references: GB:D14614; NID:g287422; PIDN:BAA03471.1; PID:g287423
 C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
 C;Genetics:
 A;Gene: VP4
 C;Superfamily: rotavirus outer layer protein VP3
 C;Keywords: hemagglutinin; outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 172
 PQ0653
 outer capsid spike protein VP4 - human rotavirus (strain AU125) (fragment)
 N;Alternate names: VP8* protein
 C;Species: human rotavirus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0653
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
 A;Reference number: PQ0651; MUID:93346985; PMID:8393919
 A;Accession: PQ0653
 A;Molecule type: mRNA
 A;Residues: 1-247 <NAK>
 A;Cross-references: GB:D14614; NID:g287410; PIDN:BAA03465.1; PID:g287411
 C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
 C;Genetics:
 A;Gene: VP4
 C;Superfamily: rotavirus outer layer protein VP3
 C;Keywords: hemagglutinin; outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 173
 PQ0657
 outer capsid spike protein VP4 - human rotavirus A (strain AU785) (fragment)
 N;Alternate names: VP8* protein
 C;Species: human rotavirus A
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
 C;Accession: PQ0657; PQ0654
 R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
 J. Gen. Virol. 74, 1709-1713, 1993
 A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
 A;Reference number: PQ0651; MUID:93346985; PMID:8393919
 A;Accession: PQ0657
 A;Molecule type: mRNA
 A;Residues: 1-247 <NAK1>
 A;Cross-references: GB:D14619; NID:g287420; PIDN:BAA03470.1; PID:g287421
 A;Experimental source: strain AU785
 A;Accession: PQ0654

A;Molecule type: mRNA
 A;Residues: 1-247 <NAK2>
 A;Cross-references: GB:D14618; NID:g287418; PIDN:BAA03469.1; PID:g287419
 A;Experimental source: strain AU720
 C;Comment: This protein plays a role in viral neutralization, viral virulence and haema
 C;Genetics:
 A;Gene: VP4
 C;Superfamily: rotavirus outer layer protein VP3
 C;Keywords: hemagglutinin; outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 174
 S61221
 outer capsid spike protein VP-8 - human rotavirus A (isolate 5193) (fragment)
 N;Alternate names: VP-8 protein
 C;Species: human rotavirus A
 A;Variety: isolate 5193
 C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
 C;Accession: S61221
 R;Gollop, R.; Kaga, E.; Silberstein, I.; Shulman, L.; Nakagomi, O.; Mendelson, E.; Shif
 submitted to the EMBL Data Library, August 1995
 A;Description: Three forms of AU-1 like viruses differentiated by their overall genomic
 A;Reference number: S61221
 A;Accession: S61221
 A;Molecule type: genomic RNA
 A;Residues: 1-247 <GOL>
 A;Cross-references: UNIPROT:Q86509; EMBL:X90733; NID:g967070; PIDN:CAAG2267.1; PID:g967
 A;Experimental source: strain AU-1; isolate 5193
 C;Genetics:
 A;Gene: VP-8
 C;Superfamily: rotavirus outer layer protein VP3
 C;Keywords: outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 199 VSSDAEF 205

RESULT 175
 S61224
 outer capsid spike protein VP-8 - human rotavirus A (isolate 6460 and others) (fragment
 N;Alternate names: VP-8 protein
 C;Species: human rotavirus A
 A;Variety: isolate 6460; isolate 6784; isolate 6584; isolate 7044
 C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
 C;Accession: S61224; S61225; S61226; S61227
 R;Gollop, R.; Kaga, E.; Silberstein, I.; Shulman, L.; Nakagomi, O.; Mendelson, E.; Shif
 submitted to the EMBL Data Library, August 1995
 A;Description: Three forms of AU-1 like viruses differentiated by their overall genomic
 A;Reference number: S61221
 A;Accession: S61224
 A;Molecule type: genomic RNA
 A;Residues: 1-247 <GOL>
 A;Cross-references: UNIPROT:Q86512; EMBL:X90736; NID:g967076; PIDN:CAAG2270.1; PID:g967
 A;Experimental source: strain AU-1; isolate 6460
 A;Accession: S61225
 A;Molecule type: genomic RNA
 A;Residues: 1-247 <GOW>
 A;Cross-references: EMBL:X90738
 A;Experimental source: strain AU-1; isolate 6784
 A;Accession: S61226

A;Molecule type: genomic RNA
A;Residues: 1-247 <GOF>
A;Cross-references: EMBL:X90737; NID:g967078; PIDN:CAA62271.1; PID:g967079
A;Experimental source: strain AU-1; isolate 6584
A;Accession: S61227
A;Molecule type: genomic RNA
A;Residues: 1-247 <GOA>
A;Cross-references: EMBL:X90739; NID:g967082; PIDN:CAA62273.1; PID:g967083
A;Experimental source: strain AU-1; isolate 7044
C;Genetics:
A;Gene: VP-8
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 199 VSSDAEF 205

RESULT 176
S61222
outer capsid spike protein VP-8 - human rotavirus A (isolate 5829 and isolate 5960) (fra
N;Alternate names: VP-8 protein
C;Species: human rotavirus A
A;Variety: isolate 5829; isolate 5960
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
C;Accession: S61222; S61223
R;Gollop, R.; Kaga, E.; Silberstein, I.; Shulman, L.; Nakagomi, O.; Mendelson, E.; Shif
submitted to the EMBL Data Library, August 1995
A;Description: Three forms of AU-1 like viruses differentiated by their overall genomic
A;Reference number: S61221
A;Accession: S61222
A;Molecule type: genomic RNA
A;Residues: 1-247 <GOL>
A;Cross-references: UNIPROT:Q86510; EMBL:X90734; NID:g967072; PIDN:CAA62268.1; PID:g9670
A;Experimental source: strain AU-1; isolate 5829
A;Accession: S61223
A;Molecule type: genomic RNA
A;Residues: 1-247 <GOW>
A;Cross-references: EMBL:X90735; NID:g967074; PIDN:CAA62269.1; PID:g967075
A;Experimental source: strain AU-1; isolate 5960
C;Genetics:
A;Gene: VP-8
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: outer capsid protein

Query Match 100.0%; Score 7; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 199 VSSDAEF 205

RESULT 177
S75632
hypothetical protein sll1892 - Synecchocystis sp. (strain PCC 6803)
C;Species: Synecchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75632
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75632

hypothetical protein sll1892 - Synecchocystis sp. (strain PCC 6803)
C;Species: Synecchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75632
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75632

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-248 <KAN>
A;Cross-references: UNIPROT:P74107; EMBL:D90912; GB:AB001339; NID:g1653228; PIDN:BAA1815
A;Experimental source: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synecchocystis hypothetical protein sll1892

Query Match 100.0%; Score 7; DB 2; Length 248;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 61 VDDQAEF 67

RESULT 178
S61960
hypothetical protein YPL107w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPG2w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61960
R;Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Vq
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: S61959
A;Accession: S61960
A;Molecule type: DNA
A;Residues: 1-248 <WAN>
A;Cross-references: UNIPROT:Q02873; EMBL:U43281; NID:g1151218; PID:g1151220; GSPDB:GN000
C;Genetics:
A;Gene: MIPS:YPL107w
A;Cross-references: SGD:S0006028
A;Map position: 16L

Query Match 100.0%; Score 7; DB 2; Length 248;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
|:::|
Db 220 VKAPAEF 226

RESULT 179
S74373
heat shock protein grpE - Synecchocystis sp. (strain PCC 6803)
N;Alternate names: hypothetical protein sll0057
C;Species: Synecchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74373
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74373

hypothetical protein sll1892 - Synecchocystis sp. (strain PCC 6803)
C;Species: Synecchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74373
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74373

hypothetical protein sll1892 - Synecchocystis sp. (strain PCC 6803)
C;Species: Synecchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75632
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75632

```
Qy      1 VXXAEF 7
        |::|||
Db     101 VALAEF 107
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RESULT 180

B64802
nagD protein - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B64802; D37018; S06991
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277. 1453-1462. 1997

```
Query Match      100.0%; Score 7; DB 1; Length 250;
Best Local Similarity 57.1%; Pred.No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels
```

Qy 1 VXXAEF 7
|::||
Db 21 VPGAEF 27

RESULT 181

AF0584
NagD protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0584
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.;
Th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.;
Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:21534947; PMID:11677608

A;Gene: STY0719
C;Superfamily: nagD protein

Query Match 100.0%; Score 7; DB 2; Length 250;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VXXAEF	7
		::	
Db	21	VGAAEF	27

RESULT 182

A90717
N-acetylglucosamine metabolism [imported] - *Escherichia coli* (strain O157:H7, substrain C); Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A90717
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen. A/Reference number: A99629; PMID:21156231; PMID:11258796

Query Match 100.0%; Score 7; DB 2; Length 250;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels

Qy 1 VXXAEF 7
|::|||
Dp 21 VPGAEF 27

RESULT 183

A85567
N-acetylglucosamine metabolism [imported] - Escherichia coli (strain O157:H7, substrain C)
Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85567
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

```
Query Match      100.0%; Score 7; DB 2; Length 250;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4: Conservative 3; Mismatches 0; Indels
```

Qy	1	VXXAEF	7
		::	
Dp	21	VPGAEF	27

RESULT 184

G87327

ABC transporter, ATP-binding subunit CC0634 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: G87327
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: G87327
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <STO>
 A:Cross-references: UNIPROT:Q9AAG6; GB:AE005673; NID:gl3421845; PIDN:AAK22619.1; GSPDB:G
 C:Genetics:
 A:Gene: CC0634

Query Match 100.0%; Score 7; DB 2; Length 250;
 Best Local Similarity 57.1%; Pred. No. 8.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 135 VDAIAEF 141

RESULT 185

AC1147
 probable conserved membrane protein lmo0578 [imported] - Listeria monocytogenes (strain
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC1147
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1147
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <GLA>
 A:Cross-references: UNIPROT:Q8Y9F1; GB:NC_003210; PIDN:CAC98657.1; PID:gl6409954; GSPDB:
 C:Genetics:
 A:Gene: lmo0578

Query Match 100.0%; Score 7; DB 2; Length 250;
 Best Local Similarity 57.1%; Pred. No. 8.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 164 VKFLAEF 170

RESULT 186

AC1506
 probable conserved membrane protein lin0587 [imported] - Listeria innocua (strain Clip11
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC1506
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1506
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <GLA>
 A:Cross-references: UNIPROT:Q92E73; GB:AL592022; PIDN:CAC95819.1; PID:gl6413027; GSPDB:
 A:Experimental source: strain Clip11262
 C:Genetics:
 A:Gene: lin0587

Query Match 100.0%; Score 7; DB 2; Length 250;
 Best Local Similarity 57.1%; Pred. No. 8.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 164 VKFLAEF 170

RESULT 187

AG2106
 hypothetical protein alr2406 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AG2106
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, I.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AG2106
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <KUR>
 A:Cross-references: UNIPROT:Q44510; GB:BA000019; PIDN:BAE74105.1; PID:gl7131498; GSPDB:
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr2406

Query Match 100.0%; Score 7; DB 2; Length 250;
 Best Local Similarity 57.1%; Pred. No. 8.3e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
 |:::|
 Db 52 VDLAEF 58

RESULT 188

B64456
 bioC protein homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004
 C:Accession: B64456
 R:Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: B64456
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-251 <BUL>
 A:Cross-references: UNIPROT:Q58648; GB:U67565; GB:L77117; NID:gl591874; PIDN:AAB99255.1.
 C:Genetics:
 A:Map position: REV1194506-1193751
 C:Superfamily: spore germination protein C2; bioC homology
 F:56-148/Domain: bioC homology <BIOC>

Query Match 100.0%; Score 7; DB 1; Length 251;

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Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
   |:::|
Db 98 VVANAEP 104

RESULT 189
A72526
hypothetical protein APE2182 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: A72526
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, AeropyrumA/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: A72526
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-251 <KAW>
A/Cross-references: UNIPROT:Q9Y9V7; DDBJ:AP000063; NID:G5105654; PIDN:BA081193.1; PID:G5A/Experimental source: strain K1
C/Genetics:
C/Superfamily: DNA polymerase sliding clamp

Query Match 100.0%; Score 7; DB 2; Length 251;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
   |:::|
Db 154 VGDFAEF 160

RESULT 190
A83660
hypothetical protein BH0081 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: A83660
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; HiraNucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans andA/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: A83660
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-251 <STO>
A/Cross-references: UNIPROT:Q9KGI0; GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA038A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH0081

Query Match 100.0%; Score 7; DB 2; Length 251;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
   |:::|
Db 165 VRPFAEF 171

RESULT 191
S59047
indole-3-glycerol phosphate synthase - Thermotoga maritima (strain MSBB)
C/Species: Thermotoga maritima
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S59047; B72414
R;Sternier, R.; Dahm, A.; Darimont, B.; Ivens, A.; Liebl, W.; Kirschner, K.

```

EMBO J. 14, 4395-4402, 1995

A:Title: (beta-alpha) (8)-barrel Proteins of tryptophan biosynthesis in the hyperthermophilic bacterium *Thermoplasma acidophilum*

A:Reference number: S59045; MUID:7556082

A:Accession: S59047

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-252 <NR>

A:Cross-references: UNIPROT:Q56319; GB:X92729; NID:g1054858; PIDN:CAA63389.1; PID:g3980

R: Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: B72414

A:Molecule type: DNA

A:Residues: 'M', 24-225, 'N', 227-252 <NR>

A:Cross-references: GB:AE001693; GB:AE000512; NID:g4980622; PIDN:AAD35233.1; PID:g49806

A:Experimental source: strain MSB8

A:Note: parts of this sequence, including the amino end of the mature protein, were det

C:Genetics:

A:Gene: trpC; TM0140

A:Start codon: ATC

C:Superfamily: indole-3-glycerol-phosphate synthase, trpC homology

F:3-247/Domain: trpC homology <TRC>

Query Match 100.0%; Score 7; DB 1; Length 252;

Best Local Similarity 57.1%; Pred. No. 8.4e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7

|:::|

Db 42 VKIIAEF 48

RESULT 192

A46505

SLA-DRAD (MHC Class II) - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A46505

F:Hirsch, F.; Germana, S.; Gustafsson, K.; Pratt, K.; Sachs, D.H.; Leguern, C.

J. Immunol. 149, 841-846, 1992

A:Title: Structure and expression of class II alpha genes in miniature swine.

A:Reference number: A46505; MUID:92340887; PMID:1634772

A:Accession: A46505

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <NR>

A:Cross-references: UNIPROT:Q31065; GB:M93028; NID:g164551; PIDN:AAA31075.1; PID:g16455

A:Note: sequence extracted from NCBI backbone (NCBIN:109901, NCBIPI:109902)

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F:123-188/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 7; DB 2; Length 252;

Best Local Similarity 57.1%; Pred. No. 8.4e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7

|:::|

Db 29 VIIQAEF 35

RESULT 193

JC2388

class II histocompatibility antigen DR alpha chain (clone W3) precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: JC2388; A37206

R:Aida, Y.; Kohda, C.; Morooka, A.; Nakai, Y.; Ogimoto, K.; Urao, T.; Asahina, M.

Biochem. Biophys. Res. Commun. 204, 195-202, 1994

A:Title: Cloning of cDNAs and the molecular evolution of a bovine MHC class II DR gene

A:Reference number: JC2388; MUID:95032095; PMID:7945359

```

A;Accession: JC2388
A;Molecule type: mRNA
A;Residues: 1-253 <AID>
A;Cross-references: UNIPROT:Q30309; UNIPROT:Q95111; DDBJ:D37956; NID:G79094
A;Experimental source: lymphoid cell line BLSC-KU-1
R;van der Poel, J.J.; Groenen, M.A.M.; Dijkhof, R.J.M.; Ruyter, D.; Giphart, M.J.
Immunogenetics 31, 29-36, 1990
A;Title: The nucleotide sequence of the bovine MHC class II alpha genes: DRA, DOA, and D
A;Reference number: A37206; MUID:90129153; PMID:2298463
A;Accession: A37206
A;Molecule type: DNA
A;Residues: 28-253 <VAN>
A;Cross-references: GB:M30120; NID:G163370; PIDN:AAA30645.1; PID:G163371
C;Genetics:
A;Introns: 82/1; 176/1
A;Superfamily: class II histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-253/Product: class II antigen DRA chain, major histocompatibility complex #status F
F;25-108/Product: alpha 1 #status predicted <AP1>
F;109-202/Product: alpha 2 #status predicted <AP2>
F;124-189/Domain: immunoglobulin homology <IMM>
F;203-215/Domain: connecting #status predicted <CNE>
F;216-239/Domain: transmembrane #status predicted <TMW>
F;240-253/Domain: intracellular #status predicted <INT>
F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 30 VIIQAEF 36

RESULT 194
S15684
MHC class II histocompatibility antigen Ovar-DR alpha chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I47075; S15684
R;Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A;Title: Isolation, characterization and evolution of ovine major histocompatibility com
A;Reference number: I47075; MUID:94057592; PMID:7902039
A;Accession: I47075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-253 <FA2>
A;Cross-references: UNIPROT:Q30828; GB:M73983; NID:G165867; PIDN:AAA16793.1; PID:G165868
C;Genetics:
A;Gene: MHC Ovar-DRA
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;124-189/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 7; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
|:::|
Db 30 VIIQAEF 36

RESULT 195
HLHDA
MHC class II histocompatibility antigen HLA-DR alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A93952; A20898; A21113; I58045; A91707; A90825; B90825; A93927; I52975; I80
R;Das, H.K.; Lawrence, S.K.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 80, 3543-3547, 1983

```

```

A;Title: Structure and nucleotide sequence of the heavy chain gene of HLA-DR.
A;Reference number: A93952; MUID:83221632; PMID:6304715
A;Accession: A93952
A;Molecule type: DNA
A;Residues: 1-254 <DAS>
A;Cross-references: UNIPROT:P01903; GB:J00203; GB:J00204; NID:G188427; PIDN:AAA36302.1;
A;Note: this allele is designated DRA*0101
R;Schambeck, A.; Korman, A.J.; Kamb, A.; Strominger, J.L.
Nucleic Acids Res. 11, 8663-8675, 1983
A;Title: Organization of the transcriptional unit of a human class II histocompatibility;
A;Reference number: A20898; MUID:84169507; PMID:6324094
A;Accession: A20898
A;Molecule type: DNA
A;Residues: 1-241,'L',243-254 <SCH>
A;Experimental source: (unknown allelotype)
R;Das, H.K.; Biro, P.A.; Cohen, S.N.; Erlich, H.A.; von Gabain, A.; Lawrence, S.K.; Lem.
Proc. Natl. Acad. Sci. U.S.A. 80, 1531-1535, 1983
A;Title: Use of synthetic oligonucleotide probes complementary to genes for human HLA-D.
A;Reference number: A21113; MUID:83169718; PMID:6403940
A;Accession: A21113
A;Molecule type: mRNA
A;Residues: 1-39 <DA2>
A;Cross-references: GB:J00197
R;Lee, J.S.; Trowsdale, J.; Travers, P.J.; Carey, J.; Grosveld, F.; Jenkins, J.; Bodmer,
Nature 299, 750-752, 1982
A;Title: sequence of an hla-dr alpha-chain cdna clone and intron-exon organization of t;
A;Reference number: I58045; MUID:83013020; PMID:6811954
A;Accession: I58045
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-254 <RES>
A;Cross-references: GB:J00194; NID:G189231; PIDN:AAA36275.1; PID:G307264
R;Das, H.K.; Lawrence, S.K.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 80, 7024, 1983
A;Reference number: A93978
A;Contents: annotation, erratum
R;Yang, C.Y.; Kratzin, H.; Gotz, H.; Thinnies, F.P.; Kruse, T.; Egert, G.; Pauly, E.; Kol
Hoppe-Seyler's Z. Physiol. Chem. 363, 671-676, 1982
A;Title: Primaerstruktur menschlicher Histokompatibilitaetsantigene der Klasse II. 2. M.
A;Reference number: A91707; MUID:82263347; PMID:6955253
A;Accession: A91707
A;Molecule type: protein
A;Residues: 26-148,'D',150-204 <VAN>
R;Barhammar, D.; Gustafsson, K.; Claesson, L.; Bill, P.; Wiman, K.; Schenning, L.; Sund
Cell 30, 153-161, 1982
A;Title: Alpha chain of HLA-DR transplantation antigens is a member of the same protein
A;Reference number: A90825; MUID:83025073; PMID:6812963
A;Accession: A90825
A;Molecule type: protein
A;Residues: 26-60 <LAR>
A;Note: 28-Ala, 29-Asp, 33-Thr, 33-Pro, 34-Tyr, 35-Pro, 48-Gln, and 54-Thr were also fo
A;Accession: B90825
A;Molecule type: mRNA
A;Residues: 32-202;204-254 <LA2>
A;Cross-references: GB:J00196
A;Note: this allele is designated DRA*0101
R;Korman, A.J.; Auffray, C.; Schambeck, A.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6013-6017, 1982
A;Title: The amino acid sequence and gene organization of the heavy chain of the HLA-DR
A;Reference number: A93927; MUID:83299916; PMID:6821129
A;Accession: A93927
A;Molecule type: DNA
A;Residues: 29-254 <KOR>
A;Cross-references: GB:J00201
A;Note: 242-Leu was also found
A;Note: this allele is designated DRA*0102
R;Kajimura, Y.; Toyoda, H.; Sato, M.; Miyakoshi, S.; Kaplan, S.A.; Ike, Y.; Goyert, S.M.
DNA 2, 175-182, 1983
A;Title: Cloning the heavy chain of human HLA-DR antigen using synthetic oligodeoxyribo
A;Reference number: I52975; MUID:84057142; PMID:6416803
A;Accession: I52975
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA

```

A;Residues: 1-254 <KAY>
A;Cross-references: GB:K011171; NID:g188264; PIDN:AAA59785.1; PID:g307267
R;Gustafsson, K.; Wiman, K.; Larhammar, D.G.; Rask, L.; Peterson, P.A.
Scand. J. Immunol. 19, 91-97, 1984
A;Title: Signal sequences distinguish class II histocompatibility antigen beta chains of
A;Reference number: I59467; MUID:84146572; PMID:6422542
A;Accession: I80355
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-50 <RE2>
A;Cross-references: GB:M35979; NID:g188262; PIDN:AAA36283.1; PID:g188263
R;Lee, J.S.; Irowdale, J.; Bodmer, W.F.
Proc. Natl. Acad. Sci. U.S.A. 79, 545-549, 1982
A;Title: cDNA clones coding for the heavy chain of human hla-dr antigen.
A;Reference number: I58984; MUID:82197531; PMID:6952207
A;Accession: I58984
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 26-42 <RE3>
A;Cross-references: GB:J00193; NID:g188213; PIDN:AAA36272.1; PID:g188214
R;Koppelman, B.; Cresswell, P.
J. Immunol. 145, 2730-2736, 1990
A;Title: Rapid nonlysosomal degradation of assembled HLA class II glycoproteins incorpo
A;Reference number: I56085; MUID:91010755; PMID:2212658
A;Accession: I56085
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-241, 'L', 243-254 <RE4>
A;Cross-references: GB:M60334; NID:g188255; PIDN:AAA59783.1; PID:g188256
R;Korman, A.J.; Knudsen, P.J.; Kaufman, J.F.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1844-1848, 1982
A;Title: cDNA clones for the heavy chain of HLA-DR antigens obtained after immunopurific
A;Reference number: I37530; MUID:82197594; PMID:6952234
A;Accession: I37530
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 224-241, 'L', 243-254 <RE6>
A;Cross-references: EMBL:V00528; NID:g32192; PIDN:CAA23787.1; PID:g825675
C;Genetics:
A;Gene: GDB:HUA-DBA
A;Cross-references: GDB:I20641; OMIM:142860
A;Map position: 6p21.3-6p21.3
A;Introns: 82/1; 176/1
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-254/Product: class II histocompatibility antigen HLA-DR alpha chain #status predict
F;26-216/Domain: extracellular #status predicted <EXT>
F;26-109/Domain: alpha-1 <EX1>
F;125-190/Domain: immunoglobulin homology <IMM>
F;217-239/Domain: transmembrane #status predicted <TSM>
F;240-254/Domain: intracellular #status predicted <INT>
F;103,143/Binding site: carboxylate (Asn) (covalent) #status experimental
F;132-188/Disulfide bonds: #status experimental

Query Match 100.0%; Score 7; DB 1; Length 254;
Best Local Similarity 57.1%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VXXAAEF 7
|:|:|:|
Db 31 VIIQAEF 37

RESULT 196
S34724
probable oxidoreductase (EC 1.1.1.-) - Serratia marcescens
C;Species: Serratia marcescens
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34724
R;Viejo, M.; Enfedaque, J.; Regue, M.
submitted to the EMBL Data Library, July 1993
A;Description: Bacteriocin 28b from Serratia marcescens does not present lysis nor immun

A;Reference number: S34724
A;Accession: S34724
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <VIE>
A;Cross-references: UNIPROT:Q54472; EMBL:Z25281; NID:g395948; PIDN:CAA80898.1; PID:g395
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
F;7-190/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 100.0%; Score 7; DB 2; Length 254;
Best Local Similarity 57.1%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VXXAAEF 7
|:|:|:|
Db 75 VSAGAEF 81

RESULT 197
G65014
hypothetical 29.2K protein b2408 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: G65014
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65014
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-254 <BLAT>
A;Cross-references: UNIPROT:P45564; GB:AB000328; GB:U00096; NID:g2367135; PIDN:AAAC75461
C;Genetics:
A;Gene: yfeN
C;Superfamily: Escherichia coli hypothetical 29.2K protein b2408

Query Match 100.0%; Score 7; DB 2; Length 254;
Best Local Similarity 57.1%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VXXAAEF 7
|:|:|:|
Db 18 VWSAEF 24

RESULT 198
T08304
sojD protein - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N;Alternate names: hypothetical protein H0991
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08304
R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: msgaplasmid or
A;Reference number: Z16408; MUID:99063795; PMID:9847077
A;Accession: T08304
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-257 <DAS>
A;Cross-references: UNIPROT:O51991; EMBL:AF016485; NID:g2822278; PID:g2822365; HALOSP: H
A;Experimental source: strain NRC-1
C;Genetics:
A;Gene: HALOSP:H0991
A;Genome: plasmid pNRC100
C;Function:
A;Description: probably involved in plasmid partitioning
C;Superfamily: regulatory protein spo0J

Job time : 31 secs

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Query Match      100.0%; Score 7; DB 2; Length 257;
Best Local Similarity 57.1%; Pred. No. 8.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |::|||
Db      77 VVAHAEF 83

RESULT 199
D82174
conserved hypothetical protein VC1641 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82174
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82174
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <HEI>
A:Cross-references: UNIPROT:Q9KRJ9; GB:AE004242; GB:AE003852; NID:g9656152; PIDN:AAF9479
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1641
A:Map position: 1

Query Match      100.0%; Score 7; DB 2; Length 257;
Best Local Similarity 57.1%; Pred. No. 8.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |::|||
Db      217 VESHAEF 223

RESULT 200
S76930
hypothetical protein slr0586 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76930
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76930
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-257 <KAN>
A:Cross-references: UNIPROT:P74722; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA1884
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

Query Match      100.0%; Score 7; DB 2; Length 257;
Best Local Similarity 57.1%; Pred. No. 8.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VXXAAEF 7
      |::|||
Db      66 VLKAEF 72
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Search completed: November 15, 2005, 10:55:40

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OM protein - protein search, using sw model

Run on: November 15, 2005, 10:50:30 ; Search time 114 Seconds
(without alignments)
31.443 Million cell updates/sec

Title: SEQ59

Perfect score: 7

Sequence: 1 vxxxaef 7

Scoring table: OLIGODX
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	17	019716	O19716 homo sapien
2	7	100.0	33	Q7UDC5	Q7UDC5 shigella fl
3	7	100.0	37	Q6M1B9	Q6M1B9 corynebacte
4	7	100.0	38	Q7M2H6	Q7M2H6 homo sapien
5	7	100.0	39	Q7M2H5	Q7M2H5 ovis aries
6	7	100.0	39	Q8F054	Q8F054 leptospira
7	7	100.0	43	Q7X3T9	Q7X3T9 xanthomonas
8	7	100.0	43	Q818G5	Q818G5 bacillus ce
9	7	100.0	46	Q88MP9	Q88MP9 pseudomonas
10	7	100.0	48	1 YGID_SCHPO	Q9P724 schizosacch
11	7	100.0	48	Q9TSA8	Q9TSA8 bos taurus
12	7	100.0	50	Q64C25	Q64C25 uncultured
13	7	100.0	50	019720	019720 homo sapien
14	7	100.0	51	Q8Q2V5	Q8Q2V5 brucella su
15	7	100.0	54	Q6QAQ7	Q6QAQ7 sus scrofa
16	7	100.0	55	Q86WB3	Q86WB3 homo sapien
17	7	100.0	55	Q92FL7	Q92FL7 listeria in
18	7	100.0	57	1 A4_URSWA	Q29149 ursus marit
19	7	100.0	58	1 A4_CANFA	Q28280 canis famil
20	7	100.0	58	1 A4_RABIT	Q28748 oryctolagus
21	7	100.0	58	1 A4_SHEEP	Q28757 ovis aries
22	7	100.0	58	Q858Q2	Q858Q2 vibrio chol
23	7	100.0	59	1 A4_BOVIN	Q28053 bos taurus
24	7	100.0	59	Q9YBN8	Q9YBN8 aeropyrum p
25	7	100.0	59	Q7N4R8	Q7N4R8 photorhabdu
26	7	100.0	60	Q93AL7	Q93AL7 clostridium
27	7	100.0	61	1 3BHS_VARV	P33794 variola vir
28	7	100.0	61	Q9QND1	Q9QND1 variola min
29	7	100.0	62	Q8KDD7	Q8KDD7 chlorobium
30	7	100.0	63	1 Y451_HABIN	P43998 haemophilus
31	7	100.0	64	2 O69895	O69895 streptomyce

32 7 100.0 65 2 Q72SU4
33 7 100.0 66 2 Q6G668
34 7 100.0 68 1 Y03B_BPT4
35 7 100.0 68 1 YB10_HALN1
36 7 100.0 70 2 Q9PGS9
37 7 100.0 73 2 Q8TJW4
38 7 100.0 73 2 Q7X1C2
39 7 100.0 74 2 Q6J931
40 7 100.0 76 1 TX3A_AGEAP
41 7 100.0 76 1 TX3B_AGEAP
42 7 100.0 77 2 Q88VS7
43 7 100.0 77 2 Q9KL79
44 7 100.0 78 1 ACP_HELPFJ
45 7 100.0 78 1 ACP_HELPFY

Q72SU4 leptospira
Q6G668 staphylococ
P32268 bacterioph
P17104 halobacteri
Q9PGS9 xylella fas
Q8TJW4 methanosa
Q7X1C2 leptospiril
Q6J931 xerophyta h
P33034 agelenopsis
P81744 agelenopsis
Q88VS7 lactobacill
Q9KL79 vibrio chol
Q9ZL81 helicobacte
P56464 helicobacte

ALIGNMENTS

RESULT 1

O19716 PRELIMINARY; PRT; 17 AA.
AC O19716;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Histocompatibility system hla-dr heavy chain. (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82197531; PubMed=6952207;
RA Lee J.S., Trowsdale J., Bodmer W.F.;
RT "CDNA clones coding for the heavy chain of human HLA-DR antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 79:545-549(1982).
DR EMBL; J00193; AAA36272.1; -;
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2058 MW; 4874E328EE649F54 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7
Db 6 VIIQAEF 12
|::|||

RESULT 2

Q7UDC5 PRELIMINARY; PRT; 33 AA.
AC Q7UDC5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical bacteriophage protein.
GN OrderedLocusNames=S0690;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;

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RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016980; AAP16173.1; -.
KW Hypochemical protein.
SQ SEQUENCE 33 AA; 3371 MW; ABC79AD62219D8E0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 11 VLTNAEF 17

RESULT 3
Q6M1B9 Q6M1B9 PRELIMINARY; PRT; 37 AA.
AC Q6M1B9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical protein.
GN OrderedLocNames-cg3434;
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
RA Kalinowski J., Bathe B., Bartels D., Bickhoff N., Bott M.,
RA Burkovski A., Dusch N., Eggeling L., Bickmanns B.J., Gaigalat L.,
RA Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
RA Tauch A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins.";
RL J. Biotechnol. 104:5-25(2003).
RW EMBL; BX927157; CAP19041.1; -.
KW Hypochemical protein.
SQ SEQUENCE 37 AA; 4308 MW; 3F99A743D5D78A98 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 37;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 27 VDNKAEF 33

RESULT 4
Q7M2H6 Q7M2H6 PRELIMINARY; PRT; 38 AA.
AC Q7M2H6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Class II histocompatibility antigen HLA-DR alpha chain
DE (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075335; PubMed=6816270;
RA Wiman K., Claesson L., Rask L., Tragardh L., Peterson P.A.;

RT "Purification and partial amino acid sequence of papain-solubilized
RT class II transplantation antigens.";
RL Biochemistry 21:5351-5358(1982).
DR PIR; A18955; A18955.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4531 MW; 9AB03C8C43B71E3D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 38;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 6 VIIQAEF 12

RESULT 5
Q7M2H5 Q7M2H5 PRELIMINARY; PRT; 39 AA.
AC Q7M2H5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Class II histocompatibility antigen 37-68 alpha chain (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=88034383; PubMed=3478413;
RA Puri N.K., Walker I.D., Brandon M.R.;
RT "N-terminal amino acid sequence analyses of the alpha-and beta-
RT polypeptides from four distinct subsets of sheep major
RT histocompatibility complex class II molecules.";
RL J. Immunol. 139:2996-3002(1987).
DR PIR; A32533; A32533.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4638 MW; 053ABD385A6388E0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 39;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
DB 6 VIIQAEF 12

RESULT 6
Q8F054 Q8F054 PRELIMINARY; PRT; 39 AA.
AC Q8F054;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LA3643;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S6601 / Serogroup Icterohaemorrhagiae / Serovar lai;

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RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interorgans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011520; AAN50841.1; -.
KW Complete proteome.
SQ SEQUENCE 39 AA; 4743 MW; AF11ED6D2C89107B CRC64;

Query Match 100.0%; Score 7; DB 2; Length 39;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 9 VGTAEF 15

RESULT 7
Q7X3T9 PRELIMINARY; PRT; 43 AA.
AC Q7X3T9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pilus biogenesis protein (Fragment).
GN NamepilB;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=XW47;
RX PubMed=15057449;
RA Yang Y.C., Chou C.P., Kuo T.T., Lin S.H., Yang M.K.;
RT "PILR enhances the sensitivity of Xanthomonas axonopodis pv. citri to
RT the infection of filamentous bacteriophage Cf.";
RL Curr. Microbiol. 48:251-261(2004).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=XW47;
RA Kou T.T., Yang Y.C., Chou C.P., Yang M.K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY295878; AAP5204.1; -.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4574 MW; D0AF93ECDF8DA62 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 43;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 15 VTSLAEF 21

RESULT 8
Q818G5 PRELIMINARY; PRT; 43 AA.
AC Q818G5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EMG2 protein.
GN OrderedLocusNames=BC4292;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).

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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017012; AAP11205.1; -.
DR InterPro; IPR003791; DUF188.
DR ProDom; PD016319; DUF188; 1.
KW Complete proteome.
SQ SEQUENCE 43 AA; 4750 MW; 25FB78686A3F5ED1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 43;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 21 VQVGAEF 27

RESULT 9
Q88MP9 PRELIMINARY; PRT; 46 AA.
AC Q88MP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PP1521;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Woestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AB016779; AAN67142.1; -.
DR TIGR; PP1521; -.
KW Complete proteome.
SQ SEQUENCE 46 AA; 5114 MW; 62P232CC3372F04E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 46;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 39 VPSLAEF 45

RESULT 10
YGID SCHPO
ID YGID_SCHPO STANDARD; PRT; 48 AA.

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AC Q9P724;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein C2A9.13 in chromosome II.
GN ORFNames=SPBC2A9.13;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby I., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler S., Wambutt R., Furnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe I., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
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CC -----
CC EMBL; AL049495; CAB66421.1; -.
DR GenBank; Spombe; SPBC2A9.13; -.
KW Hypothetical protein.
SQ SEQUENCE 48 AA; 5157 MW; DID818829D8A80CF CRC64;
  Query Match 100.0%; Score 7; DB 1; Length 48;
  Best Local Similarity 57.1%; Pred. No. 1.7e+03;
  Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
Db 21 VKKRAEF 27
  |:::|
  |:::|
RESULT 11
Q9TSA8 PRELIMINARY; PRT; 48 AA.
AC Q9TSA8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE GYRONEMIN, FILAMIN=INTERMEDIATE filament-associated protein
DE (Fragments).
  
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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92363951; PubMed=1500439;
RA Brown K.D., Binder L.I.;
RT "Identification of the intermediate filament-associated protein
RT gyronemin as filamin. Implications for a novel mechanism of
RT cytoskeletal interaction."
RT J. Cell Sci. 102:19-30 (1992).
RL InterPro; IPR001298; Filamin.
DR PROSITE; PS50194; FILAMIN_REPEAT; 1.
FT NON_TER 1 1
FT NON_CONS 25 26
FT NON_CONS 35 36
FT NON_TER 48 48
SQ SEQUENCE 48 AA; 5226 MW; 89757E2CE80A9E6E CRC64;
  Query Match 100.0%; Score 7; DB 2; Length 48;
  Best Local Similarity 57.1%; Pred. No. 1.7e+03;
  Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
Db 1 VKKRAEF 7
  |:::|
  |:::|
RESULT 12
Q64C25 PRELIMINARY; PRT; 50 AA.
AC Q64C25;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ26D6_28;
OS uncultured archaeon GZf0526D6.
OC Archaea; environmental samples.
OX NCBI_TaxID=285388;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics."
RT Science 305:1457-1462 (2004).
RL [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY14840; RAU83052.1; -.
KW Hypothetical protein.
SQ SEQUENCE 50 AA; 5819 MW; B6FB97E5F8F97A4 CRC64;
  Query Match 100.0%; Score 7; DB 2; Length 50;
  Best Local Similarity 57.1%; Pred. No. 1.7e+03;
  Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VXXXAEEF 7
Db 39 VIVQAEEF 45
  |:::|
  |:::|
RESULT 13
O19720 PRELIMINARY; PRT; 50 AA.
ID O19720;
AC O19720;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
  
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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II HLA-DR-alpha chain precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84146572; PubMed=6422542;
RA Gustafsson K., Wiman K., Larhammar D.G., Rask L., Peterson P.A.;
RT "Signal sequences distinguish Class II histocompatibility antigen beta
RT chains of different loci."
RL Scand. J. Immunol. 19:91-97(1984).
DR EMBL; M35979; AAA36283.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
KW Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 >50 Potential.
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5620 MW; 8BFF88266F8875D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 31 VIIQAEF 37

RESULT 14
Q8G2V5 PRELIMINARY; PRT; 51 AA.
AC Q8G2V5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BR0209;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1330 / Biovar 1;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kral M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Helling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014334; AAN29158.1; -.
DR TIGR; BR0209; -.
KW Complete proteome.
SQ SEQUENCE 51 AA; 5674 MW; 70C8C21A218A80AE CRC64;

Query Match 100.0%; Score 7; DB 2; Length 51;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 39 VQDGAEF 45

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RESULT 15
Q6QAQ7 PRELIMINARY; PRT; 54 AA.
AC Q6QAQ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fuse-binding protein-interacting repressor SIAHBP1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.Y., Cui X.S., Jeong Y.J., Shin M.L., Hwang K.C.; Kim N.H.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY550063; AAS55921.1; -.
FT NON_TER 1
SQ SEQUENCE 54 AA; 6102 MW; DC385DFC63C25E36 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 54;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 8 VKIFAEF 14

RESULT 16
Q86WB3 PRELIMINARY; PRT; 55 AA.
AC Q86WB3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetyl-CoA carboxylase-alpha (EC 6.4.1.2) (Fragment).
GN Name=ACACA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Travers M.T., Barber M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534888; CAD59556.1; -.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
KW Ligase.
FT NON_TER 55
SQ SEQUENCE 55 AA; 6426 MW; 8B4F39050CDAFDD8 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 55;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 44 VASPAEF 50

RESULT 17
Q92FL7 PRELIMINARY; PRT; 55 AA.
AC Q92FL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin0087 protein.
GN OrderedLocusNames=lin0087;

```

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OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Gautier K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gauthier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkut G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordbick E., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596163; CAC95320.1; -.
DR FIR; AH1443; AH1443.
DR ListList; LINO087; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6439 MW; E010C270B32A4EE0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 55;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 18 VDKLAEF 24
|::|||

RESULT 18
A4_URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q25149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC EMBL; X56128; CAA39593.1; -.
DR
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
DR Amyloid; Glycoprotein; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 Beta-amyloid protein (Potential).
FT DOMAIN <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 100.0%; Score 7; DB 1; Length 57;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 3 VKMDAEF 9
|::|||

RESULT 19
A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC EMBL; X56125; CAA39590.1; -.
DR
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
DR Amyloid; Glycoprotein; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 Beta-amyloid protein (Potential).

```

FT DOMAIN <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT NON TER 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 100.0%; Score 7; DB 1; Length 58;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 4 VKMDAEF 10

RESULT 20
 A4_RABBIT STANDARD; PRT; 58 AA.
 ID_A4_RABBIT
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 DE Name=APP;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.

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EMBL; X56129; CAA39594.1; -
 DR HSSP; P08592; INMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT CHAIN 6 48 Beta-amyloid protein (Potential).
 FT DOMAIN <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT DOMAIN 58 >58 Cytoplasmic (Potential).
 FT NON_TER 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 7; DB 1; Length 58;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

Db 3 VKMDAEF 9
 |:::|

RESULT 21
 A4_SHEEP STANDARD; PRT; 58 AA.
 ID_A4_SHEEP
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 DE Name=APP;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.

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EMBL; X56130; CAA39595.1; -
 DR HSSP; P08592; INMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT CHAIN 6 48 Beta-amyloid protein (Potential).
 FT DOMAIN <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT DOMAIN 58 >58 Cytoplasmic (Potential).
 FT NON_TER 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 7; DB 1; Length 58;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 3 VKMDAEF 9

RESULT 22
 Q858Q2 PRELIMINARY; PRT; 58 AA.
 ID Q858Q2
 AC Q858Q2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein orf58.
GN Name=orf58;
OS Vibrio cholerae phage VGph1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=223524;
RN [1]
RP SEQUENCE FROM N.A.
RA Campos J., Martinez E., Suzarte E., Rodriguez B.L., Marrero K.,
RA Silva Y.K., Ledon T.Y., Del Sol R.E., Fando R.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY242528; AAC93107.1; -.
KW Hypothetical protein.
SQ SEQUENCE 58 AA; 6317 MW; 6A3ACB367F89EFA1 CRC64;

Query Match          100.0%; Score 7; DB 2; Length 58;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 12 VCFEAF 18

RESULT 23
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog (Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)) (fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.

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EMBL; X56124; CAA39589.1; -.
DR EMBL; X56126; CAA39591.1; -.
DR HSSP; P08592; LNMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PS00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTEA; PARTIAL.
KW Amyloid; Glycoprotein; Transmembrane.

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```

FT NON_TER 1
FT CHAIN 7 49 Beta-amyloid protein (Potential).
FT DOMAIN <1 34 Extracellular (Potential).
FT TRANSMEM 25 58 Potential.
FT DOMAIN 59 >59 Cytoplasmic (Potential).
FT NON_TER 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match          100.0%; Score 7; DB 1; Length 59;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 4 VKMDAEF 10

RESULT 24
Q9YBN8
ID Q9YBN8 PRELIMINARY; PRT; 59 AA.
AC Q9YBN8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APES056.
GN ORFNames=APES056;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyana A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sakoi Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000062; BAA80560.1; -.
DR PIR; C72534; C72534.
DR InterPro; IPR006622; Znf_CDSGH.
DR SMART; SM00704; Znf_CDSGH; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 59 AA; 6540 MW; DD8F19F24F4969DF CRC64;

Query Match          100.0%; Score 7; DB 2; Length 59;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
   |::|||
Db 53 VAFEAFF 59

RESULT 25
Q7N4R8
ID Q7N4R8 PRELIMINARY; PRT; 59 AA.
AC Q7N4R8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarities with Phd protein from phage P1.
GN OrderedLocustNames=plu2254;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]

```



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RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taouit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313 (2003).
DR EMBL; BX571866; CAB14547.1; -.
DR Photolist; plu2254; -.
KW Complete proteome.
SQ SEQUENCE 59 AA; 6516 MW; A68AAB9AC568F776 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 59;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |:::|
24 VSKAEF 30

RESULT 26
Q93AL7 PRELIMINARY; PRT; 60 AA.
ID Q93AL7;
AC Q93AL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acyl-CoA dehydrogenase (EC 1.3.99.3) (Fragment).
GN Name=acda;.
OS Clostridium sporogenes.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1509;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 3584;
RA Dickert S., Pierik A.J., Buckel W.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420489; AAL18812.1; -.
DR HSP; P15651; 1UJ1.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006092; Acyl-CoA dh N.
DR InterPro; IPR009100; AcylCoA dehyd_NM.
DR Pfam; PF02771; Acyl-CoA_dh_N; 1.
KW Oxidoreductase.
FT NON_TER 60
SQ SEQUENCE 60 AA; 6949 MW; 5C5B1E3A3882752B CRC64;

Query Match 100.0%; Score 7; DB 2; Length 60;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |:::|
29 VDKTAEF 35

RESULT 27
3BHS VARV STANDARD; PRT; 61 AA.
ID 3BHS VARV
AC P33734;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Truncated 3-beta hydroxy-5-ene steroid dehydrogenase homolog.
GN Name=A501;

OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Indra-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;
RA Shchelkunov S.N., Blinov V.M., Sandakhtchiev L.S.;
RA "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83 (1993).
CC -!- SIMILARITY: Belongs to the 3beta-HSD family. Corresponds to the N-
CC terminal domain of vaccinia virus 3beta-HSD.
CC -----
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CC -----
DR EMBL; X69198; CAA49097.1; -.
DR PIR; F36853; F36853.
SQ SEQUENCE 61 AA; 6849 MW; 2563A2FAB56CCABD6 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 61;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |:::|
6 VTGGAEF 12

RESULT 28
Q9QNH1 PRELIMINARY; PRT; 61 AA.
ID Q9QNH1;
AC Q9QNH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE A54L protein.
GN Name=A54L;
OS Variola minor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=53258;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Garcia-1966;
RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Esposito J.J., Sosnovtsev S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16780; CAB34757.1; -.
DR PIR; C72170; C72170.
SQ SEQUENCE 61 AA; 6879 MW; 6463A2FAB56D11D0D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 61;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |:::|
6 VTGGAEF 12

RESULT 29
Q8KDD7 PRELIMINARY; PRT; 62 AA.
ID Q8KDD7
AC Q8KDD7;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein CT1117.
OS OrderedLocusNames=CT1117;
GN Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobaculum.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parkae D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; A2012874; AAM72350.1; -
DR TIGR; CT1117; -
KW Complete proteome.
SQ SEQUENCE 62 AA; 6811 MW; 3EA85C777A7A7D8D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 62;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 50 VIRTAEF 56

RESULT 30
Y451_HABIN STANDARD; PRT; 63 AA.
AC P43598;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein HI0451.
GN OrderedLocusNames=HI0451;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA McKenney A., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Kerkvliet A., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).

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CC -----
DR EMBL; U32728; AAC22109.1; -
DR PIR; G64007; G64007.
DR TIGR; HI0451; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 63 AA; 7047 MW; 36814E60AC306B67 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 63;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 24 VGEVAEEF 30

RESULT 31
O69895 PRELIMINARY; PRT; 64 AA.
AC O69895;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transcriptional regulator.
GN ORFNames=SC2E1.24;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Batsman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
DR EMBL; AL939124; CAA19399.1; -
DR PIR; T34792; T34792.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000192; A:amino transp.
DR InterPro; IPR000524; HTH GntR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00392; GntR; 1.
DR SMART; SM00345; HTH GNTR; 1.
DR PROSITE; PS00595; AA TRANSFER_CLASS_5; UNKNOWN_1.
DR PROSITE; PS00949; HTH GNTR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 64 AA; 6612 MW; 5A8425B3A7D7CBB1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 64;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 24 VELSAEEF 30

RESULT 32
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Q72SU4
ID Q72SU4 PRELIMINARY; PRT; 65 AA.
AC Q72SU4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=L1C11279;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhagani).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OC NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Floucriz L1-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A., Marques M.V., Oliveira M.C., Meneck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H., Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T., Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Canargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RA "Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis";
RT J. Bacteriol. 186:2164-2172(2004).
RL EMBL; AB017292; AAS69884.1; -.
RW Complete proteome.
SQ SEQUENCE 65 AA; 7750 MW; BD2D00879D520925 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 65;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VIPLAEF 11
|:::|

RESULT 33
Q6G668 PRELIMINARY; PRT; 66 AA.
AC Q6G668
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocNames=SAS2493;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OC NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.;
RA "Complete genomes of two clinical Staphylococcus aureus strains: Evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL; BX571857; CAG44309.1; -.
RW Complete proteome.
SQ SEQUENCE 66 AA; 7514 MW; 1763BE32A599EE16 CRC64;

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Query Match 100.0%; Score 7; DB 2; Length 66;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 12 VFTHAEF 18
|:::|

RESULT 34
Y03B_BPT4
ID Y03B_BPT4 STANDARD; PRT; 68 AA.
AC P32268;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 8.2 kDa protein in Gp46-Gp47 intergenic region (ORF G).
GN Name=Y03B; Synonyms=46.1;
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses
OC NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85257446; PubMed=4018026;
RA Gram H., Rueger W.;
RT "Genes 55, alpha gt, 47 and 46 of bacteriophage T4: the genomic organization as deduced by sequence analysis.";
RL EMBO J. 4:257-264(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; PubMed=12626685; DOI=10.1128/MMBR.67.1.86-156.2003;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome.";
RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
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CC -----
CC EMBL; X01804; CAA25944.1; -.
CC EMBL; AF158101; AAD42473.1; -.
CC PIR; T10161; T10161.
CC KW Hypothetical protein.
CC SEQUENCE 68 AA; 8185 MW; 54C2C72F2D52E010 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 68;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 39 VVCMAEF 45
|:::|

RESULT 35
YB10_HALN1
ID YB10_HALN1 STANDARD; PRT; 68 AA.
AC P17104; Q9H0L1;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein Vng110C (Protein NAB).
GN OrderedLocNames=VNG110C;
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.

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OX NCBI_TaxID=64091, 2242;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lesky S.K., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzel B., Keller K., Cruz R., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauer S., Kellar K., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Maddocks D.G., Jablonski P.E., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Isebnarger T.A., Peck R.F., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=H. salinarum; STRAIN=ATCC 33170 / NCCB 81095 / NRC 34001;
RX MEDLINE=89305527; PubMed=2743981;
RA Shimmin L.C., Dennis P.P.;
RT "Characterization of the L11, L1, L10 and L12 equivalent ribosomal
RT protein gene cluster of the halophilic archaeobacterium Halobacterium
RT cutirubrum.";
RL EMBO J. 8:1225-1235(1989).
CC -!- SIMILARITY: Some, to restriction endonucleases EcoRI and PstI.
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CC -----
DR EMBL; AE005042; AAG19502.1; -.
DR EMBL; X15078; CAA33177.1; -.
DR FIR; B84267; B84267.
DR FIR; S04117; QOHSNB.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 68 AA; 7539 MW; CC68625E29D3A91F CRC64;

Query Match 100.0%; Score 7; DB 1; Length 68;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 25 VDLEAEF 31
|:::|

RESULT 36
Q9PGS9 PRELIMINARY; PRT; 70 AA.
AC Q9PGS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf0219;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Arya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

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RA Pacinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.V., Martins E.A.L.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.W., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003875; AAF83032.1; -.
DR FIR; G82833; G82833.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 70 AA; 8081 MW; COA300C8624BE659 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 70;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 6 VRKSAEF 12
|:::|

RESULT 37
Q8TJW4 PRELIMINARY; PRT; 73 AA.
AC Q8TJW4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocusNames=MA3663;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr-223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Acoono D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011075; AAM07018.1; -.
KW Complete proteome.
SQ SEQUENCE 73 AA; 8467 MW; 3B02EB83569F2E34 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 73;
Best Local Similarity 57.1%; Pred. No. 2.3e+03;

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Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 51 VHWNAEF 57

RESULT 38
ID Q7X1C2 PRELIMINARY; PRT; 73 AA.
AC Q7X1C2,
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Life176p2 (Fragment).
OS Leptospirillum ferrooxidans.
OC Bacteria; Nitrospirae; Nitrospirales; Nitrospiraceae; Leptospirillum.
OC NCBI_TaxID=180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709180; PubMed=12808145; DOI=10.1073/pnas.1230487100;
RA Parro V., Moreno-Paz M.;
RT "Gene function analysis in environmental isolates: the nif regulon of
RT the strict iron oxidizing bacterium Leptospirillum ferrooxidans.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7883-7888 (2003).
DR EMBL; AY204422; AAC38379.1; -.
DR GO; GO:0009228; P:thiamin biosynthesis; IEA.
DR InterPro; IPR002817; ThiC.
DR Pfam; PF01964; ThiC; 1.
DR ProDom; PD007048; ThiC; 1.
FT NON TER 1
SQ SEQUENCE 73 AA; 8210 MW; 924D05B475E87991 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 73;
Best Local Similarity 57.1%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 21 VFKAEP 27

RESULT 39
ID Q6J931 PRELIMINARY; PRT; 74 AA.
AC Q6J931,
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xerophyta humilis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Velloziaceae; Xerophyta.
OC NCBI_TaxID=211604;
RN [1]
RP SEQUENCE FROM N.A.
RX Collett H., Illing N.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570977; AA45009.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 74 AA; 8227 MW; 0343F7C9AC2BD236 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 74;
Best Local Similarity 57.1%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 3 VTGAEP 9

RESULT 40

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TX3A_AGEAP STANDARD; PRT; 76 AA.
ID TX3A_AGEAP
AC P33034;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-agatoxin IIIA (Omega-Aga-IIIA).
OS Agelenopsis aperta (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
OC NCBI_TaxID=6908;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129351; PubMed=1310319;
RA Venema V.J., Swiderek K.M., Lee T.D., Hathaway G.M., Adams M.E.;
RT "Antagonism of synaptic calcium channels by subtypes of omega-
RT agatoxins.";
RL J. Biol. Chem. 267:2610-2615 (1992).
CC -!- FUNCTION: Omega-agatoxin are antagonist of voltage-sensitive
CC calcium channels. They block insect neuromuscular transmission
CC presynaptically. Potent blocker of N- and L-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Contains six disulfide bonds (Probable).
CC -!- SIMILARITY: Belongs to the omega-agatoxin family.
DR PIR; A42335; A42335.
KW Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
SQ SEQUENCE 76 AA; 8518 MW; 6A715CAC9591888B CRC64;

Query Match 100.0%; Score 7; DB 1; Length 76;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 42 VGTSAEF 48

RESULT 41
TX3B_AGEAP STANDARD; PRT; 76 AA.
ID TX3B_AGEAP
AC P81744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-agatoxin IIIB (Omega-Aga-IIIB).
OS Agelenopsis aperta (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
OC NCBI_TaxID=6908;
RN [1]
RP SEQUENCE, VARIANTS SER-29 AND ARG-35, AND CHARACTERIZATION.
RX TISSUE=Venom;
RX MEDLINE=94227039; PubMed=8172884;
RA Ertel E.A., Warren V.A., Adams M.E., Griffin P.R., Cohen C.J.,
RA Smith M.M.;
RT "Type III omega-agatoxins: a family of probes for similar binding
RT sites on L- and N-type calcium channels.";
RL Biochemistry 33:5098-5108 (1994).
CC -!- FUNCTION: Omega-agatoxins are antagonists of voltage-sensitive
CC calcium channels. This toxin is a potent blocker of N-type calcium
CC channels. It also blocks L-type calcium channels, but with less
CC potency than omega-Aga-IIIA. It does not block T-type channels. It
CC blocks calcium currents in locust thoracic neurones, but does not
CC block housefly neuromuscular transmission presynaptically.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Contains six disulfide bonds (Probable).
CC -!- SIMILARITY: Belongs to the omega-agatoxin family.
DR PIR; C54252; C54252.
KW Calcium channel inhibitor; Direct protein sequencing;

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KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT VARIANT 29 N -> S.
FT VARIANT 35 K -> R.
SQ SEQUENCE 76 AA; 8620 MW; D5C63C3AB8C95BB8 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 76;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
   |:|:|
Db 42 VGTSAEP 48

RESULT 42
Q88VS7 ID Q88VS7 PRELIMINARY; PRT; 77 AA.
AC Q88VS7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein lp.1960.
GN OrderedLocusNames=lp.1960;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12565656; DOI=10.1073/pnas.0337704100;
RA Kleebebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Turchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAD64344.1; -.
KW Complete proteome.
SQ SEQUENCE 77 AA; 8618 MW; C00E2BFF1D401F2F CRC64;

Query Match 100.0%; Score 7; DB 2; Length 77;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
   |:|:|
Db 65 VQLVAEP 71

RESULT 43
Q9KL79 ID Q9KL79 PRELIMINARY; PRT; 77 AA.
AC Q9KL79;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VCA0868.
GN OrderedLocusNames=VCA0868;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickley E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Baas S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
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RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004414; RAP96766.1; -.
DR FIR; E82407; E82407.
DR TIGR; VCA0868; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 77 AA; 8645 MW; 022C2BD5DEF1506F CRC64;

Query Match 100.0%; Score 7; DB 2; Length 77;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEP 7
   |:|:|
Db 32 VNTIAEP 38

RESULT 44
ACP_HELP ID ACP_HELPJ STANDARD; PRT; 78 AA.
AC Q9ZLS1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; OrderedLocusNames=JHP0506;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulphydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC
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CC
CC EMBL; AB001484; AAD06082.1; -.
CC FIR; H71922; H71922.
CC HSSP; P80643; 1F80.
CC HAMAP; MF 01217; -; 1.
CC InterPro; IPR009081; ACP_like.
CC InterPro; IPR003231; Acyl_carrier.
CC InterPro; IPR006163; Pp_bind.
CC InterPro; IPR006162; Ppantne S.
CC Pfam; PF00550; PP-binding; 1.
CC ProDom; PD000887; Acyl_carrier; 1.
CC TIGRFAMs; TIGR00517; acyl_carrier; 1.
```

DR PROSITE; PS00075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine. 36
 FT BINDING 36
 SQ SEQUENCE 78 AA; 8619 MW; B173587E30E3D811 CRC64;
 Query Match 100.0%; Score 7; DB 1; Length 78;
 Best Local Similarity 57.1%; Pred. No. 2.4e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 22 VTPEAEF 28

RESULT 45
 ACP_HELPY STANDARD; PRT; 78 AA.
 AC PS6464;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 23-OCT-2004 (Rel. 45, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN Name=acp; OrderedLocusNames=HP0559;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
 RA Dougherty B.A., Nelson K.B., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RA "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori";
 RL Nature 388:539-547(1997).
 CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC -1- PATHWAY: De novo fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acps. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulphydryl of the prosthetic group (By similarity).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.

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 CC -----
 CC EMBL; AE000570; AAD07626.1; -;
 CC F1R; G64589; G64589.
 CC HSSP; P02901; 1L0H.
 CC TIGR; HP0559; -;
 CC HAMAP; MF 01217; -; 1.
 CC InterPro; IPR009081; ACP like.
 CC InterPro; IPR003231; ACP carrier.
 CC InterPro; IPR006163; Fp_bind.
 CC InterPro; IPR006162; Pfantne S.
 CC Pfam; PF00550; PP-binding; 1.

DR ProDom; PD000887; Acyl carrier; 1.
 DR TIGRfam; TIGR00517; acyl carrier; 1.
 DR PROSITE; PS00075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine. 36
 FT BINDING 36
 SQ SEQUENCE 78 AA; 8590 MW; 5DA351914F6DCF09 CRC64;
 Query Match 100.0%; Score 7; DB 1; Length 78;
 Best Local Similarity 57.1%; Pred. No. 2.4e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 22 VTPEAEF 28

RESULT 46
 Q9NFF6 PRELIMINARY; PRT; 78 AA.
 AC Q9NFF6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative replication factor C subunit 5 (Fragment).
 GN Name=rfc5;
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=21036610; PubMed=11163452; DOI=10.1016/S0166-6851(00)00333-9;
 RA Spielmann T., Beck H.P.;
 RT "Analysis of stage-specific transcription in Plasmodium falciparum
 RT reveals a set of genes exclusively transcribed in ring stage
 RT parasites";
 RL Mol. Biochem. Parasitol. 111:453-458(2000).
 DR EMBL; A0290942; CAB92950.1; -;
 DR HSSP; Q8U4J3; 1IQP.
 FT NON TER 1
 FT NON TER 78
 SQ SEQUENCE 78 AA; 9053 MW; C2A2585155646C67 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 78;
 Best Local Similarity 57.1%; Pred. No. 2.4e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VXXAAEF 7
 Db 27 VFKADEF 33

RESULT 47
 O35463 PRELIMINARY; PRT; 79 AA.
 AC O35463;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN Name=beta APP;
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 CC NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1; -;

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DR HSSP: P08592; 1NMJ
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 79;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 18 VKMDAEF 24

RESULT 48
Q8HWZ4
ID Q8HWZ4 PRELIMINARY; PRT; 81 AA.
AC Q8HWZ4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II DR-alpha (Fragment).
GN Name=DR;
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE FROM N.A.
RA Fraser D.G., Marti E.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF541938; AAN17332.1; -.
DR HSSP: P01903; 1KLU.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0006955; P: immune response; IEA.
DR InterPro: IPR001003; MHC_II_alpha.
DR Pfam: PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9348 MW; FB12C9028F527AA8 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VIIQAEF 9

RESULT 49
Q8WM05
ID Q8WM05 PRELIMINARY; PRT; 81 AA.
AC Q8WM05;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II DR alpha 1 domain (Fragment).
GN Name=Alal-DR;
OS Alces alces (moose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Alces.
OX NCBI_TaxID=9852;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei Z., Hupp G.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR HSSP: AF458951; AAL67480.1; -.
DR HSSP: P01904; 1KTD.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0006955; P: immune response; IEA.
DR Pfam: PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9390 MW; DIFF77528EEFF7B1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VIIQAEF 9

RESULT 50
Q30455
ID Q30455 PRELIMINARY; PRT; 81 AA.
AC Q30455;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II DR-alpha (Fragment).
GN Name=DR;
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96175157; PubMed=9110935; DOI=10.1007/s002510050068;
RA Albright-Fraser D.G., Reid R., Gerber V., Bailey E.;
RL "Polymorphism of DR among equids.";
RT Immunogenetics 43:315-317(1996).
DR EMBL: I47171; AAC41631.1; -.
DR HSSP: P01903; 1KLU.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0006955; P: immune response; IEA.
DR InterPro: IPR001003; MHC_II_alpha.
DR Pfam: PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9290 MW; 5412C9005D82787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 3 VIIQAEF 9

RESULT 51
Q30459
ID Q30459 PRELIMINARY; PRT; 81 AA.
AC Q30459;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II DR-alpha (Fragment).
GN Name=DR;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
```


RX MEDLINE=96175157; PubMed=9110935; DOI=10.1007/s002510050068;
 RA Albright-Fraser D.G., Reid R., Gerber V., Bailey E.;
 RT "Polymorphism of DRA among equids.";
 RL Immunogenetics 43:315-317(1996).
 DR EMBL; L47174; AAC41630.1; --
 DR HSSP; P01903; IKLU.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001003; MHC_II_alpha.
 DR Pfam; PF00993; MHC_II_alpha; 1.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9304 MW; 504798005D850F0A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VIIQAEF 9

RESULT 52

Q30460 ID Q30460 PRELIMINARY; PRT; 81 AA.
 AC Q30460;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE DRA protein (Fragment).
 GN Name=DRA;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96175157; PubMed=9110935; DOI=10.1007/s002510050068;
 RA Albright-Fraser D.G., Reid R., Gerber V., Bailey E.;
 RT "Polymorphism of DRA among equids.";
 RL Immunogenetics 43:315-317(1996).
 DR EMBL; L47172; AAC41632.1; --
 DR HSSP; P01903; IKLU.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001003; MHC_II_alpha.
 DR Pfam; PF00993; MHC_II_alpha; 1.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9259 MW; 50478D6466650F0A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VIIQAEF 9

RESULT 53

Q30491 ID Q30491 PRELIMINARY; PRT; 81 AA.
 AC Q30491;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MHC class II DR-alpha (Fragment).
 GN Name=DRA;
 OS Equus hemionus (Kulan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96175157; PubMed=9110935; DOI=10.1007/s002510050068;
 RA Albright-Fraser D.G., Reid R., Gerber V., Bailey E.;
 RT "Polymorphism of DRA among equids.";
 RL Immunogenetics 43:315-317(1996).
 DR EMBL; L47173; AAC41633.1; --
 DR HSSP; P01903; IKLU.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001003; MHC_II_alpha.
 DR Pfam; PF00993; MHC_II_alpha; 1.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9271 MW; 5412DDBF1662787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VIIQAEF 9

RESULT 54

Q6PN75 ID Q6PN75 PRELIMINARY; PRT; 81 AA.
 AC Q6PN75;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN Name=DRA;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Senju S., Nishimura Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY591919; AAT01636.1; --
 DR HSSP; P01903; 1AQD.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR001003; MHC_II_alpha.
 DR Pfam; PF00993; MHC_II_alpha; 1.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9300 MW; E77EB88225E566DC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 3 VIIQAEF 9

RESULT 55

Q70KQ1 ID Q70KQ1 PRELIMINARY; PRT; 81 AA.
 AC Q70KQ1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MHC class II antigen (Fragment).

```
GN Name=ela-DRA;
OS Equus burchellii boehmi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=89250;
RN [1]
RN SEQUENCE FROM N.A.
RA Brown J.J., Thomson W., Clegg P.D., Eyre S., Kennedy L.J.,
RA Matthews J.B., Carter S.D., Ollier W.E.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575299; CAE01360.1; -.
DR HSSP; P01903; IAQD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9290 MW; 5412C9005D82787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |::|||
3 VIIQAEF 9

RESULT 56
Q70KQ2 PRELIMINARY; PRT; 81 AA.
ID Q70KQ2;
AC Q70KQ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=ela-DRA;
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RN SEQUENCE FROM N.A.
RA Brown J.J., Thomson W., Clegg P.D., Eyre S., Kennedy L.J.,
RA Matthews J.B., Carter S.D., Ollier W.E.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575298; CAE01359.1; -.
DR HSSP; P01903; IAQD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9290 MW; 5412C9005D82787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |::|||
3 VIIQAEF 9

RESULT 57
Q70KQ3 PRELIMINARY; PRT; 81 AA.
ID Q70KQ3;
AC Q70KQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE MHC class II antigen (Fragment).
GN Name=ela-DRA;
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RN SEQUENCE FROM N.A.
RA Brown J.J., Thomson W., Clegg P.D., Eyre S., Kennedy L.J.,
RA Matthews J.B., Carter S.D., Ollier W.E.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575297; CAE01358.1; -.
DR HSSP; P01903; IAQD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9320 MW; 49A412705D82787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |::|||
3 VIIQAEF 9

RESULT 58
Q70KQ4 PRELIMINARY; PRT; 81 AA.
ID Q70KQ4;
AC Q70KQ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=ela-DRA;
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RN SEQUENCE FROM N.A.
RA Brown J.J., Thomson W., Clegg P.D., Eyre S., Kennedy L.J.,
RA Matthews J.B., Carter S.D., Ollier W.E.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575296; CAE01357.1; -.
DR HSSP; P01903; IAQD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9306 MW; 54004B905D826765 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db |::|||
3 VIIQAEF 9

RESULT 59
Q70KQ5 PRELIMINARY; PRT; 81 AA.
ID Q70KQ5;
AC Q70KQ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=HLA-DRA;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown J.J., Thomson W., Clegg P.D., Eyre S., Kennedy L.J.,
RA Matthews J.B., Carter S.D., Ollier W.E.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575295; CAE01356.1; -.
DR HSSP; P01903; 1AQQ.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0006955; P.immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9230 MW; 5412C9005D82787A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db [:::|]
3 VIIQAEF 9

RESULT 60
Q9MXX8 PRELIMINARY; PRT; 81 AA.
AC Q9MXX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen DRA (Fragment).
OS Ovibos moschatus (Muskox).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovibos.
OX NCBI_TaxID=37176;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei Z., Happ G.M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP227193; AAF59925.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0006955; P.immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9352 MW; A6C67C1C30B5420E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db [:::|]
3 VIIQAEF 9

RESULT 61
Q9TP91 PRELIMINARY; PRT; 81 AA.
AC Q9TP91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE MHC class II antigen (Fragment).
GN Name=HLA-DRA;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawrence S.K., Ryder O.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200221; AAF12818.1; -.
DR HSSP; P01903; 1KLU.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0006955; P.immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9349 MW; E77EB88225FA76DC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db [:::|]
3 VIIQAEF 9

RESULT 62
Q98MZ8 PRELIMINARY; PRT; 81 AA.
AC Q98MZ8;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Msr0370 protein.
GN OrderedLocusNames=msr0370;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002994; BAB47965.1; -.
DR InterPro; IPR011008; Dimer_A_B_barrel.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8759 MW; 519182D79F756B8C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db [:::|]
37 VVYAEF 43

RESULT 63
Q89WL6 PRELIMINARY; PRT; 81 AA.
AC Q89WL6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bsr0662 protein.
GN OrderedLocusNames=bsr0662;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005937; BAC45927.1; -.
KW Complete proteome.
SQ SEQUENCE 81 AA; 9235 MW; D512A9FFED0DA6C7 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 40 VKVAAEF 46

RESULT 64
Q8HWJ1 ID Q8HWJ1 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Syna-DRA;
OS Syncerus caffer nanus (forest buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Syncerus.
OX NCBI_TaxID=37446;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385491; AA017918.1; -.
DR HSSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9404 MW; 34EB8CAC0F18521C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 40 VKVAAEF 46

RESULT 65
Q8HWJ2 ID Q8HWJ2 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Syna-DRA;
OS Syncerus caffer caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Syncerus.
OX NCBI_TaxID=37445;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385489; AA017916.1; -.
DR HSSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9404 MW; 34EB8CAC0F18521C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 40 VKVAAEF 46

RESULT 66
Q8HWJ3 ID Q8HWJ3 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Bula-DRA;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385489; AA017916.1; -.
DR HSSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9515 MW; D94AD32650B84D01 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 40 VKVAAEF 46

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RESULT 67
Q8HWJ4 ID Q8HWJ4 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Bula-DRA;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385488; AA017915.1; -.
DR HSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9471 MW; B235FAC650B8520A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VIIQAEF 10

RESULT 68
Q8HWJ5 ID Q8HWJ5 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Boja-DRA;
OS Bos javanicus (Wild banteng).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9906;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385487; AA017914.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9426 MW; 398E843B30B5321C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VIIQAEF 10

RESULT 69
Q8HWJ6 ID Q8HWJ6 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Boga-DRA;
OS Bos gaurus (Seladang).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9904;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385486; AA017913.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9426 MW; 398E843B30B5321C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VIIQAEF 10

RESULT 70
Q8HWJ7 ID Q8HWJ7 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Bibo-DRA;
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385485; AA017912.1; -.
DR HSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9426 MW; 398E843B30B5321C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 4 VIIQAEF 10

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Db          |:::|
4 VIIQAEF 10

Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 VXXAAEF 7
|:::|
Db          4 VIIQAEF 10

RESULT 71
Q8HWJ8
ID Q8HWJ8 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name-Ande-DRA;
OS Bubalus depressicornis (Lowland anoa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=27596;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385484; AA017911.1; -.
DR HSSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR01003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
FT NON_TER 82
SQ SEQUENCE 82 AA; 9515 MW; D94AD32650B84D01 CRC64;

Query Match      100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 VXXAAEF 7
|:::|
Db          4 VIIQAEF 10

RESULT 72
Q8HWJ9
ID Q8HWJ9 PRELIMINARY; PRT; 82 AA.
AC Q8HWJ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name-Ande-DRA;
OS Bubalus depressicornis (Lowland anoa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=27596;
RN [1]
RP SEQUENCE FROM N.A.
RA Sena L., Schneider M.P.C., Brenig B., Honeycutt R.L., Womack J.E.,
RA Skow L.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385483; AA017910.1; -.
DR HSSP; P01904; 1KTD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR01003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 82
FT NON_TER 82
SQ SEQUENCE 82 AA; 9471 MW; B235FAC650B8520A CRC64;

Query Match      100.0%; Score 7; DB 2; Length 82;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 VXXAAEF 7
|:::|
Db          4 VIIQAEF 10

Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 VXXAAEF 7
|:::|
Db          4 VIIQAEF 10

RESULT 73
Q8U2J6
ID Q8U2J6 PRELIMINARY; PRT; 83 AA.
AC Q8U2J6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0838.
GN OrderedLocusNames=PF0838;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010199; AAL80962.1; -.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 83 AA; 10024 MW; ABFD5CE7002F928C CRC64;

Query Match      100.0%; Score 7; DB 2; Length 83;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 VXXAAEF 7
|:::|
Db          38 VFDYAEF 44

RESULT 74
Q45602
ID Q45602 PRELIMINARY; PRT; 83 AA.
AC Q45602;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE YycT protein.
DE Name=YycT;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=168;
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94156824; PubMed=8113162;
RA Calogero S., Gardan R., Glaser P., Schweizer J., Rapoport G.,
RA Debarbouille M.;
RT "RocR, a novel regulatory protein controlling arginine utilization in
RT Bacillus subtilis, belongs to the NtrC/NtrA family of transcriptional
RT activators.";
RL J. Bacteriol. 176:1234-1241 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95311309; PubMed=7540694;

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RA Gardan R., Rapoport G., Debarbouille M.;
RT "Expression of the rocDEF operon involved in arginine catabolism in
RL Bacillus subtilis.";
RN J. Mol. Biol. 249:843-856 (1995).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=941171085; PubMed=8125345; DOI=10.1016/0378-1119(94)90735-8;
RA Zhang J., Aronson A.I.;
RT "A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is
RL inducible and closely linked to a NADH dehydrogenase-encoding gene.";
RN Gene 140:185-90(1994).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96093926; PubMed=7584049;
RA Yoshida K., Seki S., Fujimura M., Miwa Y., Fujita Y.;
RT "Cloning and sequencing of a 36-kb region of the Bacillus subtilis
RL genome between the gnt and iol operons.";
RN DNA Res. 2:61-69(1995).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94236234; PubMed=8180695;
RA Hartford O.M., Dows B.C.;
RT "Isolation and characterization of a hydrogen peroxide resistant
RL mutant of Bacillus subtilis.";
RN Microbiology 140:297-304(1994).
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
RT "36kb sequence between gntZ and trnY of B. subtilis genome.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78193; BAA11282.1; -.
SQ SEQUENCE 83 AA; 10084 MW; 98BF50C5490E0C83 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 83;
Best Local Similarity 57.1%; Pred.No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
Db 60 VVLRAEF 66
:::||||

RESULT 75
O62847 ID O62847 PRELIMINARY; PRT; 86 AA.
AC O62847;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Acetyl-CoA carboxylase (EC 6.4.1.2) (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=95197015; PubMed=7890176; DOI=10.1016/0378-1119(94)00871-0;
RA Barber M.C., Travers M.T.;
RT "Cloning and characterisation of multiple acetyl-CoA carboxylase
RL transcripts in ovine adipose tissue.";
RN Gene 154:271-275(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=98306048; PubMed=9639557;
RA Barber M.C., Travers M.T.;
RT "Elucidation of a promoter activity that directs the expression of

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RT acetyl-CoA carboxylase alpha with an alternative N-terminus in a
RT tissue-restricted fashion.";
RL Biochem. J. 333:17-25(1998).
DR EMBL; AJ001056; CAA04506.1; -.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005481; CPase L.N.
DR Pfam; PF00289; CPase_L_chain; 1.
KW Ligase.
FT NON_TER 86
SQ SEQUENCE 86 AA; 9906 MW; 8F43EA0F92743378 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 86;
Best Local Similarity 57.1%; Pred.No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
Db 44 VASPAEF 50
:::||||

RESULT 76
Q6N8B1 ID Q6N8B1 PRELIMINARY; PRT; 87 AA.
AC Q6N8B1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Possible virulence-associated protein.
GN OrderedLocusNames=RPA1993;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572599; CAE27434.1; -.
DR InterPro; IPR007159; SpvT_AbrB.
DR Pfam; PF04014; SpvT_AbrB; 1.
KW Complete proteome.
SQ SEQUENCE 87 AA; 9921 MW; AE9554162E4BC899 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 87;
Best Local Similarity 57.1%; Pred.No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXXXAEF 7
Db 17 VRLPAEF 23
:::||||

RESULT 77
Q854J0 ID Q854J0 PRELIMINARY; PRT; 88 AA.
AC Q854J0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp74.
OS Mycobacteriophage Omega.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205879;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=127059866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandaamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RA "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AV129338; AN12718.1; -.
SQ SEQUENCE 88 AA; 10324 MW; 5D13C1010CA6985E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 88;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 50 VSVAAEF 56
|:::|

RESULT 78
Q6YVE3 PRELIMINARY; PRT; 88 AA.
AC Q6YVE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein B1120F06.135 (Hypothetical protein
DE B1272H04.1)
GN Name=B1120F06.135; Synonyms=B1272H04.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:B1120F06.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:B1272H04.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005930; BAC84533.1; -.
DR EMBL; AF006479; BAD32057.1; -.
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 10001 MW; 693B4D3224B4D010 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 88;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 52 VVATAEF 58
|:::|

RESULT 79
Q8IF91 PRELIMINARY; PRT; 89 AA.
AC Q8IF91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Tb927.1.2950.
GN Name=Tb927.1.2950;
OS Trypanosoma brucei.
OC Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma.

```

```

OX NCBI_TaxID=5691;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Barriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA Bart-Delabesse E.N., Gerrare C.S., Atkin R.J., Barron A.J., Bowman S.,
RA Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch E.,
RA Reitter C., Rutherford K., Sasse J., Sharp S., Showkeen R.,
RA Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA Barrell B., Melville S.E.;
RT "The DNA sequence of chromosome I of an African trypanosome: gene
RT content, chromosome organisation, recombination and polymorphism.";
RL Nucleic Acids Res. 31:4864-4873(2003).
DR EMBL; AL929605; CAD53150.1; -.
KW Hypothetical protein.
SQ SEQUENCE 89 AA; 10046 MW; BB4ED11C43E9DCD2 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 89;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
Db 30 VIVFAEF 36
|:::|

RESULT 80
ES6C_MYCTU STANDARD; PRT; 90 AA.
ID ES6C_MYCTU
AC 005441;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Putative ESAT-6 like protein 12.
GN OrderedLocustNames=RV3904c, MT4023; ORFNames=MTCV15F10.07;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekaita F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh M.A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
CC -!- SIMILARITY: Belongs to the ESAT-6 (esx) family.
CC -----
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CC EMBL; BX842584; CAB08097.1; -;
 DR EMBL; AE000516; AAK48387.1; -;
 DR PIR; A70600; A70600.
 DR TIGR; MT4023; -;
 DR TubercuList; RV3904c; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 9603 MW; 83AB18F16E023B9E CRC64;

Query Match 100.0%; Score 7; DB 1; Length 90;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 10 VARMAEF 16

RESULT 81

Q73SS4 ID Q73SS4 PRELIMINARY; PRT; 90 AA.
 AC Q73SS4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP3999c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017241; AAS06549.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 9871 MW; 8158A349D8C264B3 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 10 VQMAEF 16

RESULT 82

Q7TVD7 ID Q7TVD7 PRELIMINARY; PRT; 90 AA.
 AC Q7TVD7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PUTATIVE ESAT-6 LIKE PROTEIN 12 (HYPOTHETICAL ALANINE RICH PROTEIN).
 GN Name=esx6; OrderedLocusNames=MbJ934c;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AF2122/97;
 RL MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of Mycobacterium bovis";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 DR EMBL; BX248347; CAD96120.1; -;
 DR EMBL; BX248347; CAD96120.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 9571 MW; 9E1C18F16E023B9E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 10 VARMAEF 16

RESULT 83

Q7W5G2 ID Q7W5G2 PRELIMINARY; PRT; 90 AA.
 AC Q7W5G2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ferredoxin.
 GN OrderedLocusNames=BPP3330;
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12822 / ATCC BAA-587;
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640433; CAE38615.1; -;
 DR HSSP; P00214; 1FRK.
 DR GO; GO:0005489; F1electron transporter activity; IEA.
 DR GO; GO:0005506; F1iron ion binding; IEA.
 DR GO; GO:0006118; F1electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR Pfam; PF00037; Fer4; 1.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 90 AA; 10073 MW; 759358DEB5735518 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 56 VELSAEF 62

RESULT 84

Q7WCZ7 ID Q7WCZ7 PRELIMINARY; PRT; 90 AA.
 AC Q7WCZ7;

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferredoxin.
GN OrderedLocusNames=BB3781;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagers K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Skelton J., Squares R., Squares S., Stevens K.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640448; CAE35755.1; -.
DR HSSP; P00214; IPRK.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fex4; 1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 90 AA; 10073 MW; 759358DEB5735518 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 56 VELSAEF 62

RESULT 85
Q81207 PRELIMINARY; PRT; 90 AA.
AC Q81207; Q613V2; Q6KJB9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Prophage LambdaBa04, DNA packaging protein, putative.
GN OrderedLocusNames=BA0470, BSA0448, GBAA0470;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=127212629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillye L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.B., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;

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RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative Genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017025; AAP24495.1; -.
DR EMBL; AE017334; AAT35268.1; -.
DR EMBL; AE017225; AAT52779.1; -.
DR TIGR; BA0470; -.
DR TIGR; GBAA0470; -.
DR InterPro; IPR006450; DUF_DNA_pack.
DR TIGRFAMs; TIGR01560; put_DNA_pack; 1.
KW Complete proteome.
SQ SEQUENCE 90 AA; 10181 MW; 317D17E4D1444514 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 56 VYCKAEF 62

RESULT 86
Q9L381 PRELIMINARY; PRT; 90 AA.
AC Q9L381;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE NtrP protein (NITROGEN REGULATORY PROTEIN).
OS Name=ntrP; ORFNames=Smc03949;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21330262; PubMed=11437262;
RA Olah B., Kiss E., Gyorgypal Z., Borzi J., Cinege G., Csanadi G.,
RA Batut J., Kondorosi A., Dusha I.;
RT "Mutation in the ntrP gene, a member of the vap gene family, increases
RT the symbiotic efficiency of Sinorhizobium meliloti.";
RL Mol. Plant Microbe Interact. 14:887-894(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Fumelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AJ277847; CAB90829.1; -.
DR EMBL; AL591790; CAC46996.1; -.

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DR InterPro; IPR007159; SpOVT_AbrB.
 DR Pfam; PF04014; SpOVT_AbrB; 1.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 10334 MW; 208E8735DE1BCBE4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 90;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 24 VRIPAEF 30

RESULT 87

O8KPS3 PRELIMINARY; PRT; 91 AA.
 AC O8KPS3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein SEF0021.
 GN Name=SEF0021;
 OS *Synechococcus* sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7492;
 RA Holtman C.K., Sandoval P., Chen Y., Socias T., Mohler B.J.,
 RA McMurtry S., Gonzalez A., Salinas I., Golden S.S., Youderian P.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY120853; AA82696.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 91 AA; 10246 MW; 1568E2D3359B1F82 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 91;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 36 VLHPAEF 42

RESULT 88

O8VMP3 PRELIMINARY; PRT; 91 AA.
 AC O8VMP3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS *Pseudomonas putida*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22423065; PubMed=12534468;
 RA Greated A., Lamberton L., Williams P.A., Thomas C.M.;
 FT "Complete sequence of the IncP-9 TOL plasmid pW0 from *Pseudomonas putida*."
 RL Environ. Microbiol. 4:856-871 (2002).
 DR EMBL: AJ344068; CAC86746.1; -
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 91 AA; 10325 MW; 314F73E8672166CA CRC64;

Query Match 100.0%; Score 7; DB 2; Length 91;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 70 VDRIAEF 76

RESULT 89

PR10 CAVPO STANDARD; PRT; 92 AA.
 AC P20658;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein 10 (29 kDa calcium-binding protein, brain-specific)
 DE (Fragments).
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Brain;
 RX MEDLINE=9009311; PubMed=2602362;
 RA Winsky L., Nakata H., Martin B.M., Jacobowitz D.M.;
 RT "Isolation, partial amino acid sequence, and immunohistochemical
 RT localization of a brain-specific calcium-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:10139-10143 (1989).
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- MISCELLANEOUS: Binds calcium.
 CC -1- SIMILARITY: Belongs to the calbindin family.
 CC -1- SIMILARITY: Contains 6 EF-hand calcium-binding domains.
 DR PIR; A34520; A34520.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DE PROSITE; PS00018; EF_HAND; PARTIAL.
 KW Calcium-binding; Direct protein sequencing.
 FT NON_TER 1 1
 FT NON_CONS 17 18
 FT NON_CONS 27 28
 FT NON_CONS 41 42
 FT NON_CONS 76 77
 FT NON_CONS 82 83
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 11067 MW; D1CCD66C148A7F6A CRC64;

Query Match 100.0%; Score 7; DB 1; Length 92;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
 |:::|
 Db 30 VGSSAEF 36

RESULT 90

O814U6 PRELIMINARY; PRT; 92 AA.
 AC O814U6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BC5323;
 OS *Bacillus cereus* (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 Overbeek R., Kyrpides N.C.;

RT "Genome sequence of *Bacillus cereus* and comparative analysis with
 RT *Bacillus anthracis*.";
 RL Nature 423:87-91(2003).
 DR EMBL; AB017015; AAP12186.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 92 AA; 10815 MW; 217C03619E8F601A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 92;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 24 VQFAEF 30

RESULT 91

Q8D7X4 PRELIMINARY; PRT; 92 AA.
 AC Q8D7X4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Rhodanese-related sulfurtransferase.
 GN OrderedLocusNames=VV20022;
 OS *Vibrio vulnificus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016808; IGMX.
 DR HSSP; P09390; IGMX.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001763; Rhodanese-like.
 DR Pfam; PF00581; Rhodanese; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANES_3; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 92 AA; 10226 MW; C2EB44A0B5D539B3 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 92;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 16 VRTPAEF 22

RESULT 92

Q7Z2M2 PRELIMINARY; PRT; 93 AA.
 AC Q7Z2M2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE BA436C9.2 (PUTATIVE novel protein similar to part of HSP70/HSP90
 DE organizing protein and transformation sensitive protein)
 DE (Fragment).
 GN Name=BA436C9_2;
 OS *Homo sapiens* (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark G.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL121825; CAB81628.1; -.
 DR HSSP; P31948; IELW.
 DR InterPro; IPR001440; TPR.
 DR InterPro; IPR008941; TPR-like.
 DR PROSITE; PS50293; TPR_REGION; 1.
 FT NON_TER 1
 FT NON_TER 93
 SQ SEQUENCE 93 AA; 10390 MW; 56563795A5BDD347 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 93;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 18 VLSKAEF 24

RESULT 93

O81131 PRELIMINARY; PRT; 94 AA.
 AC O81131;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Aspartic proteinase inhibitor (Fragment).
 GN Name=API-1;
 OS *Cucurbita maxima* (Pumpkin) (Winter squash).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 OX NCBI_TaxID=3661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Phloem;
 RX MEDLINE=98314517; PubMed=9652409;
 RA Christeller J.T., Farley P.C., Ramsay R.J., Sullivan P.A., Laing W.A.;
 RT "Purification, characterization and cloning of an aspartic proteinase
 RT inhibitor from squash phloem exudate.";
 RL Eur. J. Biochem. 254:160-167(1998).
 DR EMBL; AF038166; AAC39473.1; -.
 DR PIR; T08058; T08058.
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
 FT NON_TER 1
 SQ SEQUENCE 94 AA; 10352 MW; 91E49AEA7817EA36 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 18 VKEIAEF 24

RESULT 94

O81132 PRELIMINARY; PRT; 94 AA.
 AC O81132;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Aspartic proteinase inhibitor (Fragment).
 GN Name=API-2;
 OS *Cucurbita maxima* (Pumpkin) (Winter squash).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 OX NCBI_TaxID=3661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Phloem;

RX MEDLINE=98314517; PubMed=9652409;
 RA Christeller J.T., Farley P.C., Ramsay R.J., Sullivan P.A., Laing W.A.,
 RT "Purification, characterization and cloning of an aspartic proteinase
 inhibitor from squash phloem exudate.";
 RL Eur. J. Biochem. 254:160-167(1998).
 DR EMBL; AF038167; AAC39474.1; -;
 DR PIR; T08062; T08062.
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
 FT NON TER
 SQ SEQUENCE 94 AA; 10359 MW; 91E492C2D542A45A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 18 VKSIAEF 24

RESULT 95

Q630S5 ID Q630S5 PRELIMINARY; PRT; 94 AA.
 AC Q630S5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Group-specific protein.
 GN ORFNames=BTZK5023;
 OS Bacillus cereus ZK.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=288681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZK;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus cereus ZK";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CP000001; AAU15257.1; -;
 SQ SEQUENCE 94 AA; 11066 MW; 8E3BBC691AE9A84E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 27 VQMAEF 33

RESULT 96

Q6HAW0 ID Q6HAW0 PRELIMINARY; PRT; 94 AA.
 AC Q6HAW0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BT9727.5007;
 OS Bacillus thuringiensis (Subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=180856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-27;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017355; AAT63002.1; -;

KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 94 AA; 11094 MW; 8E3BAEE21AE9A84E CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 94;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 Db 27 VQMAEF 33

RESULT 97

ES6X MYCLE STANDARD; PRT; 95 AA.
 ID ES6X MYCLE
 AC Q49946;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Putative ESAT-6 like protein X.
 GN OrderedLocusNames=ML1056; ORFNames=ul756d;
 GN and
 GN OrderedLocusNames=ML1180; ORFNames=MLCB1701.06c;
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
 RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
 RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jageis K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 CC -1- SIMILARITY: Belongs to the ESAT-6 (esx) family.

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EMBL; U15180; AAC62902.1; -;
 EMBL; AL049191; CAB39146.1; -;
 EMBL; AL583920; CAC31437.1; -;
 EMBL; AL583921; CAC31561.1; -;
 DR PIR; T45170; T45170.
 DR Leproma; ML1056; -;
 DR Leproma; ML1180; -;
 DR InterPro; IPR009416; DUF1066.
 DR Pfam; PF06359; DUF1066; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 95 AA; 10260 MW; 2DA8F0F5B698F20B CRC64;

Query Match 100.0%; Score 7; DB 1; Length 95;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

```
Db 36 VRDAEF 42 |:::|
|:::|
RESULT 98
Q7Q392 PRELIMINARY; PRT; 95 AA.
AC Q7Q392;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP11425 (Fragment).
GN Name=agCG53860; ORFNames=ENSANGG00000007856;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008964; EAA12806.1; -.
DR GO; GO:0004129; P:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004204; COX6C.
DR Pfam; PF02937; COX6C; 1.
DR ProDom; PD015032; COX6C; 1.
DR NON_TER 1
FT SEQUENCE 95 AA; 10696 MW; E4147B64D99FD4FA CRC64;
SQ

Query Match 100.0%; Score 7; DB 2; Length 95;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7 |:::|
DB 65 VRDYAEF 71 |:::|

RESULT 99
O52913 PRELIMINARY; PRT; 95 AA.
AC O52913;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 90 (Fragment).
GN Name=htp9;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=NCTC 11168;
RA Karlyshev A.V., Wren B.W.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ000963; CAA04340.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Heat shock.
KW NON_TER 1
FT SEQUENCE 95 AA; 10546 MW; 886B9FE51CAB1D69 CRC64;
SQ

Query Match 100.0%; Score 7; DB 2; Length 95;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7 |:::|
DB 65 VRDYAEF 71 |:::|

Db 76 VDNPAEF 82 |:::|
|:::|
RESULT 100
O6YY08 PRELIMINARY; PRT; 96 AA.
AC O6YY08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNB0056122.43 (Hypothetical protein
DE OSJNB0046012.3).
GN Name=OSJNB0056122.43; Synonyms=OSJNB0046012.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RC SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005644; BAD17492.1; -.
DR EMBL; AP005643; BAD17440.1; -.
KW Hypothetical protein.
SQ SEQUENCE 96 AA; 10556 MW; 8A5DEE863B23C461 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 96;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7 |:::|
DB 13 VDTAEF 19 |:::|

RESULT 101
Q89WX7 PRELIMINARY; PRT; 96 AA.
AC Q89WX7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bsl0551 protein.
GN OrderedLocusNames=bsl0551;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideasa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005936; BAC45816.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003425; Unk_YGFT.
DR Pfam; PF02325; YGFT; 1.
KW Complete proteome.
SQ SEQUENCE 96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 96;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7 |:::|
```

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Db      41 VSAVAEF 47
|:::|
RESULT 102
YBGA_THEME
ID YBGA_THEME STANDARD; PRT; 98 AA.
AC Q08640;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein in Bgla 3'-region (ORF2) (Fragment).
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OC NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=94104595; PubMed=8277941;
RA Liebl W., Gabelsberger J., Schleifer K.H.;
RT "Comparative amino acid sequence analysis of Thermotoga maritima beta-
glucosidase (Bgla) deduced from the nucleotide sequence of the gene
RT indicates distant relationship between beta-glucosidases of the Bga
family and other families of beta-1,4-glycosyl hydrolases.";
RL Mol. Gen. Genet. 242:111-115(1994).
CC -!- CAUTION: As the DNA coding for this protein is not found in the
CC complete genome of T.maritima. It could have originated from
CC another bacterial species.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74163; CAA52277.1; -
DR PIR; S41562; S41562.
KW Hypothetical protein.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11094 MW; 6869278434858370 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 86 VWPAAEF 92

RESULT 103
Q6AF18
ID Q6AF18 PRELIMINARY; PRT; 98 AA.
AC Q6AF18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=lx11810;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Microbacteriaceae; Leifsonia.
OC NCBI_TaxID=59736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,

Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
Goldman G.H., Kimura E.T., Perro E.S., Kuramae E.E., Lenos E.G.M.,
Lenos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza J.A.,
Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT89027.1; -
KW Complete proteome.
SQ SEQUENCE 98 AA; 10182 MW; 567C76F4FFBC365D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 68 VIGFAEF 74

RESULT 104
Q94M09
ID Q94M09 PRELIMINARY; PRT; 99 AA.
AC Q94M09;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P14.
OS Bacteriophage phi-12.
OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX NCBI_TaxID=161736;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22031230; PubMed=12033785; DOI=10.1006/viro.2002.1436;
RT Gottlieb P., Potgieter C., Wei H., Toporovsky I.;
RT "Characterization of phi12, a bacteriophage related to phi6:
RT nucleotide sequence of the large double-stranded RNA.";
RL Virology 295:266-271(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Gottlieb P.J., Potgieter C., Wei H., Toporovsky I.;
RA Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF408636; AAL01104.1; -
SQ SEQUENCE 99 AA; 11485 MW; 91C57108570E53F1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 99;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
|:::|
Db 79 VHLTAEF 85

RESULT 105
Q9LX28
ID Q9LX28 PRELIMINARY; PRT; 100 AA.
AC Q9LX28;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T5P19_70.
GN Name=T5P19_70;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopeis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Wurmback E., Drzonek H., Ansoerge W., Mewes H.W., Rudd S.,

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RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL163972; CAB88045.1; -
DR PIR: T49043; T49043.
DR HSSP: P10599; ITRV.
DR GO: GO:0005489; P:electron transport activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006662; ThioRed.
DR InterPro: IPR006663; ThioRedox_dom2.
DR Pfam: PF00085; ThioRedoxin; 1.
DR PRINTS: PR00421; THIOREDXIN.
KW Hypothetical protein; Redox-active center.
SQ SEQUENCE 100 AA; 11269 MW; 9EFC0C5980386EB CRC64;

Query Match 100.0%; Score 7; DB 2; Length 100;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 47 VEELAEF 53

RESULT 106
SPT4 KLULA
ID SPT4_KLULA STANDARD; PRT; 102 AA.
AC P81205;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Transcription initiation protein SPT4.
GN Names=SPT4; OrderedLocNames=KLUA0B07997g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=JBD100;
RX MEDLINE=99087905; PubMed=98711119;
RA Hikkei I., Gbelska Y., Subik J.;
RT "Identification and functional analysis of a Kluyveromyces lactis
homologue of the SPT4 gene of Saccharomyces cerevisiae.";
RN Curr. Genet. 34:375-378(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Fairhead C., Confanioli F., de Daruvar A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.-L., Sudeau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -1- FUNCTION: Important for transcription initiation. The SPT4/5/6
complex is required for transcription initiation. It may normally
act to repress transcription at a variety of loci, and also plays
a role in chromatin structure or assembly. Metal binding is
important for its function (By similarity).
CC

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CC -1- SUBUNIT: Complex of SPT4, SPT5 and SPT6 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC
DR EMBL: CR382122; CAH02279.1; -
DR InterPro: IPR009287; Spt4.
DR Pfam: PF06093; Spt4; 1.
KW Nuclear protein; Transcription; Zinc-finger.
FT ZN FING 7 27 By similarity.
SQ SEQUENCE 102 AA; 11224 MW; 869070285CF7917C CRC64;

Query Match 100.0%; Score 7; DB 1; Length 102;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 13 VQSTAEF 19

RESULT 107
Q6DKU9
ID Q6DKU9 PRELIMINARY; PRT; 102 AA.
AC Q6DKU9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aspartic protease inhibitor.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
[1]
RP SEQUENCE FROM N.A.
RA Anandan A., Christeller J., Marshall R., Allan A.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Anandasayanan A.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY672634; AAT72725.1; -
DR GO: GO:0008233; F:peptidase activity; IEA.
KW Protease.
SQ SEQUENCE 102 AA; 11145 MW; 77D95B5ADB18DBC4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
Db 26 VKEIAEF 32

RESULT 108
Q6DLC8
ID Q6DLC8 PRELIMINARY; PRT; 102 AA.
AC Q6DLC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aspartic protease inhibitor.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 RN NCBI_TaxID=3661;
 RP SEQUENCE FROM N.A.
 RA Anandan A., Farley P., Wright M., Christeller J., Laigne W.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RP Anandasayanan A.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY666083; AAT67162.1; -;
 DR GO; GO:0008233; F:peptidase activity; IEA.
 KW Protease.
 SQ SEQUENCE 102 AA; 11161 MW; 1BD95B5ADB18DBD4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
 Best Local Similarity 57.1%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 DB 26 VKSIAEF 32
 |:::|

RESULT 109

ID O6DLC9 PRELIMINARY; PRT; 102 AA.
 AC O6DLC9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Aspartic protease inhibitor.
 OS Cucurbita maxima (Pumpkin) (Winter squash).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 OC NCBI_TaxID=3661;
 RN SEQUENCE FROM N.A.
 RP Anandan A., Farley P., Wright M., Christeller J., Laigne W.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RA Anandasayanan A.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY666082; AAT67162.1; -;
 DR GO; GO:0008233; F:peptidase activity; IEA.
 KW Protease.
 SQ SEQUENCE 102 AA; 11267 MW; 740566B70A1665DB CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
 Best Local Similarity 57.1%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 DB 26 VKSIAEF 32
 |:::|

RESULT 110

ID Q741L6 PRELIMINARY; PRT; 102 AA.
 AC Q741L6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP1074c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1770;
 RN SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017230; AAS03391.1; -;
 KW Complete proteome.
 SQ SEQUENCE 102 AA; 11579 MW; 57D645815C8B2378 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
 Best Local Similarity 57.1%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 DB 83 VIDVAEF 89
 |:::|

RESULT 111

ID Q81R27 PRELIMINARY; PRT; 102 AA.
 AC Q81R27; Q6HZ97; Q6KT91;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BA2232, BAS2078, GBAA2232;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1392;
 RN SEQUENCE FROM N.A.
 RP STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin N., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzaple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.D., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koshler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RT Nature 423:81-86(2003).
 RN SEQUENCE FROM N.A.
 RP STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics."
 RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RP STRAIN=Scerne;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AS017031; AAP26109.1; -;
 DR EMBL; AS017334; AAT31352.1; -;
 DR EMBL; AS017225; AAT54392.1; -;
 DR TIGR; BA2232; -;
 DR TIGR; GBAA2232; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
 Best Local Similarity 57.1%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VXXAAEF 7
Db 51 VDEVAEF 57

RESULT 112
Q68358
ID Q68358 PRELIMINARY; PRT; 102 AA.
AC Q68358;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=EUBAH3485;
RX MEDLINE=96030859; PubMed=7595353;
RA Mellor J., Holmes E.C., Jarvis L.M., Yap P.L., Simmonds P.,
RA The Int'l HCV Collaborative Study Group;
RT "Investigation of the pattern of hepatitis C virus sequence diversity
RT in different geographical regions: implications for virus
RT classification.";
RL J. Gen. Virol. 76:2493-2507(1995).
DR EMBL; U31254; AAV75058.1; -.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 10407 MW; E3B0611FF5980B35 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 102;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 19 VLSAEF 25

RESULT 113
Q96859
ID Q96859 PRELIMINARY; PRT; 103 AA.
AC Q96859;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein signaling regulator EAR-16 (fragment).
GN Name=eat-16;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=21231612; PubMed=1133232;
RA van Der Linden A.M., Simmer F., Cuppen E., Plasterk R.H.A.;
RT "The G Protein beta Subunit GPB-2 in Caenorhabditis elegans Regulates
RT the G(alpha)-G(q)alpha Signaling Network Through Interactions With
RT the Regulator of G Protein Signaling Proteins EGL-10 and EAT-16.";
RL Genetics 158:221-235(2001).
DR EMBL; AF291851; AAK59598.1; -.
DR GO; GO:0005834; C:heterotrimeric G-protein complex; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0001770; G-gamma.
DR InterPro; IPR001770; G-gamma.
DR SMART; SM00631; G-gamma; 1.
DR SMART; SM00224; GGL; 1.
FT NON_TER 1 1
FT NON_TER 103 103
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SQ SEQUENCE 103 AA; 11983 MW; 4D8B13BC7489F617 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 37 VDOAEF 43

RESULT 114
Q82U10
ID Q82U10 PRELIMINARY; PRT; 103 AA.
AC Q82U10;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DUF190.
GN OrderedLocusNames=NEI703;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]_TaxID=915;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321862; CAD85614.1; -.
DR InterPro; IPR003793; DUF190.
DR Pfam; PF02641; DUF190; 1.
SQ Complete proteome.
KW SEQUENCE 103 AA; 11694 MW; 905A03DA0ED0669E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 93 VKVAAEF 99

RESULT 115
Q88P15
ID Q88P15 PRELIMINARY; PRT; 103 AA.
AC Q88P15;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PP1038;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]_TaxID=160488;
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Meinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
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RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016777; AAN66663.1; -.
DR TIGR; PP1038; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 103 AA; 11364 MW; 76D3DCFCFA37D6F6 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 103;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 97 VWRLAEF 103
|:|:|:|:|

RESULT 116
Q7KQL8 PRELIMINARY; PRT; 104 AA.
AC Q7KQL8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12358864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shalton S.J., Suh B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511 (2002).
DR EMBL; AE014825; AAN37158.1; -.
DR HSSP; P10599; IAU.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 97 VWRLAEF 103
|:|:|:|:|

RESULT 117
Q9NFK9 PRELIMINARY; PRT; 104 AA.
ID Q9NFK9
AC Q9NFK9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12358864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shalton S.J., Suh B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511 (2002).
DR EMBL; AE014825; AAN37158.1; -.
DR HSSP; P10599; IAU.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 97 VWRLAEF 103
|:|:|:|:|

RESULT 118
Q7WYS6 PRELIMINARY; PRT; 104 AA.
ID Q7WYS6
AC Q7WYS6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Rhizobium leguminosarum bv. viciae 3841.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium;
OC Rhizobium leguminosarum bv. viciae.
OX NCBI_TaxID=216596;
RN [1]
RP SEQUENCE FROM N.A.
RA Kannenberg E.L., Mueller P., Brewin N.J., Schmitz S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ571701; CAE00201.1; -.
KW Hypothetical protein.
SQ SEQUENCE 104 AA; 11614 MW; B621CDB998EC19A2 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 4 VSDPAEF 10
|:|:|:|:|

RESULT 119
Q6G4L9 PRELIMINARY; PRT; 105 AA.
ID Q6G4L9
AC Q6G4L9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277839; CAB90828.1; -.
DR HSSP; P80028; 1EP7.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VTSQAEF 11
|:|:|:|:|

RESULT 119
Q6G4L9 PRELIMINARY; PRT; 105 AA.
ID Q6G4L9
AC Q6G4L9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277839; CAB90828.1; -.
DR HSSP; P80028; 1EP7.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VTSQAEF 11
|:|:|:|:|

RESULT 119
Q6G4L9 PRELIMINARY; PRT; 105 AA.
ID Q6G4L9
AC Q6G4L9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277839; CAB90828.1; -.
DR HSSP; P80028; 1EP7.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VTSQAEF 11
|:|:|:|:|

RESULT 119
Q6G4L9 PRELIMINARY; PRT; 105 AA.
ID Q6G4L9
AC Q6G4L9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277839; CAB90828.1; -.
DR HSSP; P80028; 1EP7.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VTSQAEF 11
|:|:|:|:|

RESULT 119
Q6G4L9 PRELIMINARY; PRT; 105 AA.
ID Q6G4L9
AC Q6G4L9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277839; CAB90828.1; -.
DR HSSP; P80028; 1EP7.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR006663; Thioedox_dom2.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR TIGRFAMs; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 104;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 5 VTSQAEF 11
|:|:~::~|||

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DE Hypothetical prophage protein.
GN OrderedLocusNames-BH03220;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49882 / Houston 1;
RA PubMed=15210978; DOI=10.1073/pnas.0305659101;
RX Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardeall D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27133.1; -.
DR InterPro; IPR008651; HicB.
DR InterPro; IPR010985; Met_repress_like.
DR Pfam; PF05534; HicB; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 105 AA; 11959 MW; 40AB0B6098ECB518 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 105;
Best Local Similarity 57.1%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3;

QY 1 VXXAAEF 7
|:::|
DB 20 VGLCAEF 26

RESULT 120
Q9BGL5 ID Q9BGL5 PRELIMINARY; PRT; 106 AA.
AC Q9BGL5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Matrilysin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=21858324; PubMed=11870075;
RA Rieke W.A., Smith G.W., Smith M.F.;
RT "Matrix metalloproteinase expression and activity following
RT prostaglandin F(2 alpha)-induced luteolysis.";
RL Biol. Reprod. 66:685-691(2002).
DR EMBL; AF267158; AAG59846.1; -.
DR HSP; P09237; LMW.
DR MEROPS; M10.008; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00235; ZnMc; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11578 MW; EBD271054928018 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 106;
Best Local Similarity 57.1%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3;

QY 1 VXXAAEF 7
|:::|
DB 20 VGLCAEF 26

RESULT 121
Q6BA79 ID Q6BA79 PRELIMINARY; PRT; 106 AA.
AC Q6BA79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Uncultured proteobacterium eBACred25D05.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=287841;
RN [1]_
RP SEQUENCE FROM N.A.
RA Oz A., Sabehi G., Koblizek M., Massana R., Beja O.;
RT "Roseobacter-like bacteria in Red and Mediterranean Sea aerobic
RT anoxygenic photosynthetic populations.";
RL Appl. Environ. Microbiol. 0:0-0(2004).
DR EMBL; AY671989; RAT90292.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006660; Arsen_reductase.
DR Pfam; PF03960; Arsc; 1.
KW Hypothetical protein.
SQ SEQUENCE 106 AA; 12069 MW; F07F2BD3885B700E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 106;
Best Local Similarity 57.1%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3;

QY 1 VXXAAEF 7
|:::|
DB 18 VLQSAEF 24

RESULT 122
Q8GGE3 ID Q8GGE3 PRELIMINARY; PRT; 106 AA.
AC Q8GGE3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Streptomyces sp. EN27.
OG Plasmid pEN2701.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=211464;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=EN27;
RX MEDLINE=22472596; PubMed=12584005; DOI=10.1016/S0147-619X(02)00153-1;
RA Coombs J.T., Franco C.M.M., Loria R.;
RT "Complete sequencing and analysis of pEN2701, a novel 13-kb plasmid
RT from an endophytic Streptomyces sp.";
RL Plasmid 49:86-92(2003).
DR EMBL; AF533985; AAN76283.1; -.
DR Hypothetical protein; Plasmid.
SQ SEQUENCE 106 AA; 11488 MW; E2B127026C785A91 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 106;
Best Local Similarity 57.1%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3;

QY 1 VXXAAEF 7
|:::|
DB 94 VAAQAEF 100

RESULT 123

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Q89166
ID Q89166 PRELIMINARY; PRT; 106 AA.
AC Q89166
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulatory protein.
GN OrderedLocusNames=bl15773;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shingo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RL DNA Res. 9:189-197(2002).
CC -1- SIMILARITY: Contains 1 HTH arsr-type DNA-binding domain.
DR EMBL; AP005956; BAC1038.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001845; WHH_Arsr.
DR InterPro; IPR009058; WHH_hlx_DNA_bnd.
DR Pfam; PF01022; HTH 5; 1.
DR PRINTS; PR00778; HTHARSR.
DR SMART; SM00418; HTH ARSR; 1.
DR Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 106 AA; 11935 MW; A96FB2B423F14B6A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 106;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 41 VGBLAEP 47

RESULT 124
Q6MDY7 PRELIMINARY; PRT; 106 AA.
ID Q6MDY7
AC Q6MDY7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=pc0488;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Besser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA Rattai T., Newes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RL the evolutionary history of chlamydiae."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAP23212.1; -.
DR InterPro; IPR000182; GCN5acetyl trans.
DR Pfam; PF00583; Acetyltransf.1; I.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 106 AA; 12083 MW; 1CCDB63A50A1533E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 106;

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Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 60 VAGFAEF 66

RESULT 125
Q7VTF8 PRELIMINARY; PRT; 107 AA.
ID Q7VTF8
AC Q7VTF8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferredoxin.
GN OrderedLocusNames=BP3582;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohana I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Farraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Bagham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RL Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640421; CAE43841.1; -.
DR HSSP; P00214; IF5B.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 107 AA; 12012 MW; 3FC8C5D43BE1DA6D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 107;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 73 VELSAEF 79

RESULT 126
Q9PCU3 PRELIMINARY; PRT; 107 AA.
ID Q9PCU3
AC Q9PCU3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf1662;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Bueno M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorzy H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier J.M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quadrio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.W., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidiana J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003992; AAF84471.1; -.
DR FIR: A82653; A82653.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 107 AA; 11951 MW; 3E20A8702514A8F2 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 107;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 86 VLFGAEEF 92
|:::|

RESULT 127
Q8CB91 PRELIMINARY; PRT; 107 AA.
AC Q8CB91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus adult male bone cDNA, RIKEN full-length enriched library,
DE clone:9830132L24 product:hypothetical protein, full insert
DE sequence.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Hirozane T.,
RA Kurihara C., Matsuyama T., Miyazaki R., Kondo S., Konno H., Kouda M., Koya S.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK036546; BAC29471.1; -.
KW Hypothetical protein.
SQ SEQUENCE 107 AA; 12753 MW; 71D44B9CDBF79BA8 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 107;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEEF 7
DB 24 VLSTAEF 30
|:::|

RESULT 128
YF24_METJA STANDARD; PRT; 108 AA.
AC Q58919;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical UPF0166 protein M31524.
GN OrderedLocustNames=MJ1524;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT Jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: Belongs to the UPF0166 family.
CC -----
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CC -----
DR EMBL; U67593; AAB99550.1; -.
DR PIR; C64490; C64490.
DR TIGR; MJ1524; -.
DR InterPro; IPR003793; DUF190.
DR Pfam; PF02641; DUF190; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF8B CRC64;

Query Match 100.0%; Score 7; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
   |:::|
Db 49 VRGVAEF 55

RESULT 129
VMTM_LAMB
ID VMTM_LAMB STANDARD; PRT; 109 AA.
AC P03737;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Minor tail protein M.
GN Name=M;
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10710;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83189071; PubMed=6221115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RA "Nucleotide sequence of bacteriophage lambda DNA."
RL J. Mol. Biol. 162:729-773(1982).
CC -!- FUNCTION: Gene M protein is a minor tail protein, located at the
CC distal end, and is involved in the assembly of the initiator
CC complex for tail polymerization. It acts to stabilize the complex.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02459; AAA96549.1; -.
DR PIR; I43008; TLBPML.

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DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
SQ SEQUENCE 109 AA; 12530 MW; 4D19F7308377DCA9 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
   |:::|
Db 98 VEFSAEF 104

RESULT 130
ID 059465 PRELIMINARY; PRT; 109 AA.
AC 059465;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PH1801.
DE OrderedLocusNames=PF1801.
GN OrderedLocusNames=PF1801;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]_TaxID=53953;
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:555-76(1998).
DR EMBL; AF000007; BAA30920.1; -.
DR PIR; A71191; A71191.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005538; LrgA.
DR Pfam; PF03788; LrgA; 1.
DR ProDom; PD009239; LrgA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 109 AA; 11912 MW; 206BF04FCFF70532 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXXAEF 7
   |:::|
Db 49 VERAEF 55

RESULT 131
Q87ZY1
ID Q87ZY1 PRELIMINARY; PRT; 109 AA.
AC Q87ZY1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PF1844.
DE OrderedLocusNames=PF1844;
GN OrderedLocusNames=PF1844;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.

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```

RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
RL "The complete sequence of the Pyrococcus furiosus genome.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010280; AAL81968.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR Pfam; PF03788; LrgA; 1.
DR ProDom; PD009239; LrgA; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 11991 MW; 0C3816C9C49303AB CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 49 VEKEAEF 55

RESULT 132
Q9VIR7 PRELIMINARY; PRT; 109 AA.
AC Q9VIR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative effector of murein hydrolase LrgA.
GN ORFNames=PA80239;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GE5 / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
DR EMBL; AJ248284; CAB49282.1; -.
DR PIR; C75150; C75150.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR005538; LrgA.
DR Pfam; PF03788; LrgA; 1.
DR ProDom; PD009239; LrgA; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 109 AA; 11607 MW; 38BD644F2703BD60 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 49 VEKEAEF 55

RESULT 133
Q687F2 PRELIMINARY; PRT; 109 AA.
AC Q687F2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative tail fiber component M.
GN ORFNames=EC CP1639_57;
OS Bacteriophage CP-1639.
OC Viruses.

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OX NCBI_TaxID=291401;
RN [1]
RP SEQUENCE FROM N.A.
RA Creuzburg K., Koehler B., Hempel H., Schreier P. Jacobs E.,
RA Schmidt H.;
RT "Genetic structure and chromosomal integration site of the cryptic
Shiga toxin 1-converting prophage CP-1639.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Creuzburg K.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304858; CAH23255.1; -.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
SQ SEQUENCE 109 AA; 12614 MW; 0BFBB301A5959F5E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 98 VEFSAEF 104

RESULT 134
Q8X305 PRELIMINARY; PRT; 109 AA.
AC Q8X305;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Minor tail protein.
GN OrderedLocusNames=ECs1644;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002555; BAB35067.1; -.
DR PIR; D90834; D90834.
DR Pfam; PF05939; Phage_min_tail; 1.
SQ SEQUENCE 109 AA; 12458 MW; ESC511329E2397A6 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 98 VEFSAEF 104

RESULT 135
Q986I2 PRELIMINARY; PRT; 109 AA.
AC Q986I2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE M117344 protein.
GN OrderedLocusNames=m117344;

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OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099; PubMed=11214968;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF003011; BAB53471.1; -.
DR InterPro; IPR006311; Tat.
DR TIGRPFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 11482 MW; F297217262B95AC3 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.le+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 99 VFQTAEF 105
|:::|

RESULT 136
Q8FEW9 PRELIMINARY; PRT; 109 AA.
ID Q8FEW9
AC Q8FEW9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative tail component of prophage.
DE Minor tail protein M (Putative tail component of prophage CP-9330)
DE (Putative tail fiber component M of prophage CP-9330)
GN OrderedLocustNames=c3159;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016759; AAN79930.1; -.
DR PIR; C85817; C85817.
DR PIR; D90969; D90969.
DR PIR; D90997; D90997.
DR PIR; E90899; E90899.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12614 MW; OBPBB301A5959F5E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.le+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 98 VEFSAEF 104
|:::|

RESULT 137
Q8FEW9 PRELIMINARY; PRT; 109 AA.
ID Q8FEW9
AC Q8FEW9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative tail component of prophage.
DE Minor tail protein M (Putative tail component of prophage CP-9330)
DE (Putative tail fiber component M of prophage CP-9330)
GN OrderedLocustNames=c3159;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=20564182; PubMed=11111050; DOI=10.1016/S0378-1119(00)00416-9;
RX Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
RA Yotsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
RA Shingawa H.;
RT "Complete nucleotide sequence of the defective Sakai-V71 prophage
RT carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
RT coli O157:H7 derived from the Sakai outbreak.";
RL Gene 258:127-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=0174935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

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ID Q8FIG1 PRELIMINARY; PRT; 109 AA.
AC Q8FIG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative tail fiber component M of prophage.
DE OrderedLocustNames=c1461;
GN Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016759; AAN79930.1; -.
DR PIR; C85817; C85817.
DR PIR; D90969; D90969.
DR PIR; D90997; D90997.
DR PIR; E90899; E90899.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12614 MW; OBPBB301A5959F5E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.le+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 98 VEFSAEF 104
|:::|

RESULT 138
Q8FEW9 PRELIMINARY; PRT; 109 AA.
ID Q8FEW9
AC Q8FEW9;
DT 01-MAR-2003 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Minor tail protein M (Putative tail component of prophage CP-9330)
DE (Putative tail fiber component M of prophage CP-9330)
GN OrderedLocustNames=ECs2165, ECs2724, ECs2948, Z2141, Z3083;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20564182; PubMed=11111050; DOI=10.1016/S0378-1119(00)00416-9;
RX Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
RA Yotsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
RA Shingawa H.;
RT "Complete nucleotide sequence of the defective Sakai-V71 prophage
RT carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
RT coli O157:H7 derived from the Sakai outbreak.";
RL Gene 258:127-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=0174935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

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RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AP000400; BAB19567.1; -
DR EMBL; AE005349; AAG56207.1; -
DR EMBL; AE005420; AAG56999.1; -
DR EMBL; AP002557; BAB35588.1; -
DR EMBL; AP002559; BAB36147.1; -
DR EMBL; AP002560; BAB36371.1; -
DR PIR; C85817; C85817.
DR PIR; D90969; D90969.
DR PIR; D90997; D90997.
DR PIR; E90899; E90899.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12614 MW; 0BFBB301A5959F5E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 98 VFSAEF 104

RESULT 139
QBX4W8 ID Q8X4W8 PRELIMINARY; PRT; 109 AA.
AC Q8X4W8; Q7AFX8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative tail component of prophage CP-933R (Putative minor tail
DE protein).
GN OrderedLocusNames=EC61115, 22353;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Hayaashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005368; AAG56399.1; -
DR EMBL; AP002554; BAB34538.1; -
DR PIR; C85742; C85742.
DR PIR; C90768; C90768.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR010265; Phage_min_tail.
DR Pfam; PF05939; Phage_min_tail; 1.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12740 MW; 806BAD13FDAADA8E CRC64;

Query Match 100.0%; Score 7; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 98 VFSAEF 104

RESULT 140
O33004 ID O33004 PRELIMINARY; PRT; 110 AA.
AC O33004;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MLCB2492.25.
GN Name=MLCB2492.25;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=93188700; PubMed=8446027;
RA Biglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
RT "Use of an ordered cosmid library to deduce the genomic organization
RT of Mycobacterium leprae."
RL Mol. Microbiol. 7:197-206(1993).
RN [2]
SEQUENCE FROM N.A.
RA Cole S.T., Flesselles B., Honore N.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBSJ databases.
DR EMBL; Z98756; CAB11457.1; -
DR PIR; T45387; T45387.
KW Hypothetical protein.
SQ SEQUENCE 110 AA; 11872 MW; 3694872BBAD5B57C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 110;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXXAEF 7
DB 92 VGEAAEF 98

RESULT 141
Q7V725 ID Q7V725 PRELIMINARY; PRT; 111 AA.
AC Q7V725;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PMT0937;
OS Prochlorococcus marinus (strain MIT 9313).

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Q9LBP6
ID Q9LBP6 PRELIMINARY; PRT; 113 AA.
AC Q9LBP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase form I large subunit
DE (fragment).
GN Name=Rubisco cbbL;
OS uncultured deep-sea autotrophic bacterium OTI-9.
OC Bacteria; environmental samples.
OX NCBI_TaxID=117029;
RN [1]_TaxID=117029;
RP SEQUENCE FROM N.A.
RX MEDLINE=21178529; PubMed=11282630;
RX DOI=10.1128/AEM.67.4.1751-1765.2001;
RA Elsaied H., Naganuma T.;
RT "Phylogenetic diversity of ribulose-1,5-bisphosphate
RT carboxylase/oxygenase large-subunit genes from deep-sea
RT microorganisms.";
RL Appl. Environ. Microbiol. 67:1751-1765(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Elsaied H.E., Naganuma T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the RuBisCO large chain family.
DR EMBL; AB038637; BAA92483.1; -.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR InterPro; IPR000685; RuBisCO_large.
DR Pfam; PF00016; RuBisCO_large; 1.
DR PROSITE; PS00157; RUBISCO_LARGE; 1.
FT NON_TER 1 1
FT TER 113 113
SQ SEQUENCE 113 AA; 12679 MW; 294C3086F12FD418 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 113;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 63 VLKRAEF 69

RESULT 146
Q65L36 PRELIMINARY; PRT; 113 AA.
ID Q65L36;
AC Q65L36;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein xkdd.
GN Name=xkdd; ORFNames=BL03833, BLi01324;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 13;
RX PubMed=15383718;
RA Veitch B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaia P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,

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RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU40228.1; -.
DR EMBL; CP000002; AAU22876.1; -.
KW Hypothetical protein.
SQ SEQUENCE 113 AA; 12949 MW; AE0B58B8FA6ACD52 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 113;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 101 VVAKAEF 107

RESULT 147
Q72XC9 PRELIMINARY; PRT; 113 AA.
ID Q72XC9;
AC Q72XC9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE5449;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017281; AAS44349.1; -.
DR TIGR; BCE5449; -.
KW Complete proteome.
SQ SEQUENCE 113 AA; 13362 MW; FD18E4731C25422A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 113;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 46 VQMPAEF 52

RESULT 148
Q87H95 PRELIMINARY; PRT; 113 AA.
ID Q87H95;
AC Q87H95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VPA1070.
GN OrderedLocusNames=VPA1070;
OS Vibrio parahaemolyticus
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

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RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62413.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 113 AA; 12837 MW; 67115258261E888D CRC64;

Query Match 100.0%; Score 7; DB 2; Length 113;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 60 VAIGAEF 66

RESULT 149
Q8JH58 PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AN04908.1; -.
DR HSP; Q61013; IYT.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03454; Beta_APP; 1.
DR PRINTS; PR0203; AMYLOIDR4.
DR PRINTS; PR0204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 113;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 12 VKMDAEF 18

RESULT 150
Q67S45 PRELIMINARY; PRT; 114 AA.
ID Q67S45;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=STH513;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]

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RP SEQUENCE FROM N.A.
RA STRAIN=IAM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD39498.1; -.
DR InterPro; IPR001310; HIT.
DR Pfam; PF01230; HIT; 1.
DR PRINTS; PR00332; HISTRIAD.
DR PROSITE; PS00892; HIT; 1.
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12265 MW; 89D5EFADB3F1CF04 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 114;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 48 VPSVAEF 54

RESULT 151
Q81JX7 PRELIMINARY; PRT; 114 AA.
ID Q81JX7; Q6QH7; Q6QV1;
AC Q81JX7; Q6QH7; Q6QV1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA5566, BAS5172, GBAA5566;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12716229; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RN Nature 423:81-86(2003).
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RC Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RC Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RC Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Stearns;
RC Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RC Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017041; AAP29209.1; -.
DR EMBL; AB017334; AAT34709.1; -.
DR EMBL; AB017225; AAT57461.1; -.
DR TIGR; BA5566; -.

```

DR TIGR; GBAA5566; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 114 AA; 13529 MW; 2775972BC30D9147 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 114;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAFF 7
Db 46 VQWFAEF 52
|:::|
|:::|

RESULT 152
Q91EY3 PRELIMINARY; PRT; 114 AA.
AC Q91EY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF72.
GN Cydia pomonella granulosis virus (CpGV) (Cydia pomonella
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=28289;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=96207404; PubMed=8615018; DOI=10.1006/viro.1996.0175;
RA Theilmann D.A., Chanler J.K., Stewart S., Flipsen H.T., Vlak J.M.,
RA Crook N.E.;
RT "Characterization of a highly conserved baculovirus structural protein
RT that is specific for occlusion-derived virions.";
RL Virology 218:148-158(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=97380577; PubMed=9237352; DOI=10.1023/A:1007917317770;
RA Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
RT "Complete sequence and transposon mutagenesis of the BamHI J fragment
RT of Cydia pomonella granulosis virus.";
RL Virus Genes 14:131-136(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=93188168; PubMed=8445726;
RA Crook N.E., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
RT motif.";
RL J. Virol. 67:2168-2174(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=98418511; PubMed=9747739;
RA Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.;
RT "Identification and characterization of the Cydia pomonella
RT granulovirus cathepsin and chitinase genes.";
RL J. Gen. Virol. 79:2283-2292(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=2146686; PubMed=11562546;
RA Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RT "The complete sequence of the Cydia pomonella granulovirus genome.";
RL J. Gen. Virol. 82:2531-2547(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RA Kang W.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.

RC STRAIN=Mexican 1;
RA Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53466; AAK70732.1; -.
SQ SEQUENCE 114 AA; 13768 MW; 4F005D4BE147EBD7 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 114;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 68 VNSFAEF 74
|:::|
|:::|

RESULT 153
Q8A172 PRELIMINARY; PRT; 116 AA.
AC Q8A172;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BT3794;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OX Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016942; AAO78899.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 116 AA; 11869 MW; DFAC729A3C3B9FAC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 116;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 110 VAASAEF 116
|:::|
|:::|

RESULT 154
Q64UA1 PRELIMINARY; PRT; 118 AA.
AC Q64UA1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Thioredoxin.
GN ORFNames=BF2181;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OX Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006841; BAD48928.1; -.
SQ SEQUENCE 118 AA; 13423 MW; 8F5CFB0C9EDDB132 CRC64;

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Query Match      100.0%; Score 7; DB 2; Length 118;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 12 VKVAEF 18

RESULT 155
Q8T0J6 PRELIMINARY; PRT; 119 AA.
AC Q8T0J6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GH26763p.
GN NamesOda; Synonyms=guf; (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Aebayani A., Carlson J.,
RA Chame M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069220; AAL39365.1; -.
DR FlyBase; FBgn0014184; Oda.
DR GO; GO:0007422; P:peripheral nervous system development; NAS.
SQ SEQUENCE 119 AA; 13850 MW; 7B5604A4F2B7B4C4 CRC64;

Query Match      100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 69 VVAAEF 75

RESULT 156
Q95YG4 PRELIMINARY; PRT; 119 AA.
AC Q95YG4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Novel protein (Spermathecal expression protein 1).
GN Namessth-1; ORFNames=ZC513.12;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Bando T., Ikeda T., Kagawa H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=Bristol N2;
RA Wu X., Le T.T.;
RT "The sequence of C. elegans cosmid ZC513.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072927; BAB69890.1; -.
DR EMBL; U53155; AAM48562.1; -.
DR WormBase; WBGene00006060; sth-1.
DR WormPep; ZC513.12; CS31137.
SQ SEQUENCE 119 AA; 13530 MW; 3BB5A41B007A7E7B CRC64;

Query Match      100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 19 VFPVAF 25

RESULT 157
Q853J0 PRELIMINARY; PRT; 119 AA.
AC Q853J0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp90.
OS Mycobacteriophage Bx1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Fedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182 (2003).
DR EMBL; AY129337; AAN16747.1; -.
SQ SEQUENCE 119 AA; 13047 MW; 312DBF653F853587 CRC64;

Query Match      100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VXXAAEF 7
Db 5 VDVAEF 11

RESULT 158

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Q859E0
ID Q859E0 PRELIMINARY; PRT; 119 AA.
AC Q859E0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Pseudomonas phage gh-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=197783;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22728229; PubMed=12842620; DOI=10.1016/S0042-6922(03)00124-7;
RA Kovalyova I.V., Kropinski A.M.;
RT "The complete genomic sequence of lytic bacteriophage gh-1 infecting
RT Pseudomonas putida-evidence for close relationship to the T7 group.";
RL Virology 311:305-315(2003).
DR EMBL; AF493143; AAO73175.1; -.
KW Hypothetical protein.
SQ SEQUENCE 119 AA; 13550 MW; 571E07F06D00226A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 30 VMLTAEF 36

RESULT 159
Q9C9E1
ID Q9C9E1 PRELIMINARY; PRT; 119 AA.
AC Q9C9E1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein T10D10.10.
GN NamesT10D10.10;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016529; AAG52573.1; -.
DR EMBL; AY088935; AAM67240.1; -.
DR PIR; D96748; D96748.
DR InterPro; IPR003676; Auxin_inducible.
DR Pfam; PF02519; Auxin_inducible; 1.

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KW Hypothetical protein.
SQ SEQUENCE 119 AA; 13591 MW; 054929837114222C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 110 VEELAEF 116

RESULT 160
Q87BC8
ID Q87BC8 PRELIMINARY; PRT; 119 AA.
AC Q87BC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderdiococcusNames=PD1529;
OS Xylella fastidiosa (strain Temeculal / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
RA Miyaki C.Y., Furian L.R., Camargo L.E.A., da Silva A.C.R., da Silva F.R.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Camman F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa.";
RL J. Bacteriol. 185:1018-1026(2003).
DR EMBL; AE012558; AAO29371.1; -.
KW Complete proteome.
SQ SEQUENCE 119 AA; 13564 MW; 7DEA9F603BE3BBAF CRC64;

Query Match 100.0%; Score 7; DB 2; Length 119;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 107 VKRIAEP 113

RESULT 161
Q722G8
ID Q722G8 PRELIMINARY; PRT; 120 AA.
AC Q722G8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Acetyl-CoA carboxylase 1 (fragment).
GN Name=ACCI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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SEQUENCE FROM N.A.
RP MEDLINE=22709197; PubMed=12810950; DOI=10.1073/pnas.1332670100;
RA Mao J., Chirala S.S., Wakil S.J.;
RT "human acetyl-CoA carboxylase 1 gene: presence of three promoters and
RL heterogeneity at the 5'-untranslated mRNA region.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7515-7520(2003).
DR EMBL; AY315621; AAP94116.1; -.
DR EMBL; AY315623; AAP94118.1; -.
DR EMBL; AY315625; AAP94120.1; -.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13062 MW; 89A777CF5248CB12 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 120;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 102 VASPAEF 108

RESULT 162
YIF9_YEAST STANDARD; PRT; 121 AA.
AC P40520;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical 13.0 kDa protein in SNPI-GPPI intergenic region.
GN OrderedLocusNames=YIL059C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313266; PubMed=9169870;
RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moulle S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL Nature 387:84-87(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97313266; PubMed=9169870;
RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moulle S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,
RA LaBaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomycetes
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL; Z38060; CAA86164.1; -.
DR EMBL; AY693258; AAT93277.1; -.
DR FTR; S48420; S48420.
DR Germline; 139596; -.
DR SGD; S000001321; YIL059C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 7 23 Potential.
SQ SEQUENCE 121 AA; 13030 MW; 18B23D652939CDD2 CRC64;

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Query Match 100.0%; Score 7; DB 1; Length 121;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 19 VTALAEF 25

RESULT 163
Q05388 PRELIMINARY; PRT; 121 AA.
AC Q05388;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orf 06150 protein.
GN Name=orf 06150;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=97051589; PubMed=8896266;
RX DOI=10.1002/(SICI)1097-0061(199609)12:10B<1021::AID-YEA981>3.3.CO;2-Z;
RA Pearson B.M., Hernando Y., Payne J., Wolf S.S., Kalogeropoulos A.,
RA Schweizer M.;
RT "Sequencing of a 35.71 kb DNA segment on the right arm of yeast
RT chromosome XV reveals regions of similarity to chromosomes I and
RT XIII.";
RL Yeast 12:1021-1031(1996).
DR EMBL; X90565; CAA62177.1; -.
DR FTR; S72002; S58332.
SQ SEQUENCE 121 AA; 13252 MW; F3B3075CB9BEA6FC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 121;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
   |:::|
Db 55 VALIAEF 61

RESULT 164
Q6ZTT7 PRELIMINARY; PRT; 122 AA.
AC Q6ZTT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ44232.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Oesaki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuoka K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK126220; BAC86492.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
KW ATP-binding.

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SQ SEQUENCE 122 AA; 14313 MW; C8BE3965589230DD CRC64;
Query Match 100.0%; Score 7; DB 2; Length 122;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 24 VLFLAEF 30

RESULT 165
Q8TU11 ID Q8TU11 PRELIMINARY; PRT; 123 AA.
AC Q8TU11;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocusNames=WA3803;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnr H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002);
DR EMBL; AE011092; AM07154.1; -.
KW Complete proteome.
SQ SEQUENCE 123 AA; 12789 MW; D71653938D1DFB4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 123;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 17 VEATAEF 23

RESULT 166
Q6YUAS ID Q6YUAS PRELIMINARY; PRT; 123 AA.
AC Q6YUAS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein B1116H04.30.
GN Name=B1116H04.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005871; BAD10695.1; -.
KW Hypothetical protein.
SQ SEQUENCE 123 AA; 14250 MW; 49517FC761CD65E4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 123;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 13 VDRTAEF 19

RESULT 167
Q6CE02 ID Q6CE02 PRELIMINARY; PRT; 124 AA.
AC Q6CE02;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity (Fragment).
GN ORFNames=YALIOB19778g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boirane A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerret A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellissier S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA Swenne D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382128; CAG83363.1; -.
FT NON_TER 1
SQ SEQUENCE 124 AA; 12591 MW; 049DB4403A3BCC05 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 124;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|::|||
Db 29 VPSDAEF 35

RESULT 168
Q853C8 ID Q853C8 PRELIMINARY; PRT; 124 AA.
AC Q853C8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp154.
GN Name=154;

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OS Mycobacteriophage Bx21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2252660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Hout J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AV129337; AAN16809.1; -
DR HSSP; Q9V3E5; 107S.
SQ SEQUENCE 124 AA; 13428 MW; E405AF0C3474999B CRC64;

Query Match 100.0%; Score 7; DB 2; Length 124;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 28 VHAAEF 34

RESULT 169
O8GAUO PRELIMINARY; PRT; 124 AA.
AC O8GAUO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA Gyrase subunit A (Fragment).
GN Name=gyrA;
OS Wolbachia endosymbiont of Callosobruchus chinensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_TaxID=188349;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WBruAus;
RA MEDLINE=22294998; PubMed=12386340; DOI=10.1073/pnas.222228199;
RA Kondo N., Nikoh N., Iijichi N., Shimada M., Fukatsu T.;
RT "Genome fragment of Wolbachia endosymbiont transferred to X chromosome
of host insect.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14280-14285(2002).
DR EMBL; AB081842; BAC22722.1; -
DR HSSP; P09097; 1AB4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR002205; DNA_topoisomIV.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00434; TOP4c; 1.
FT NON_TER 124 124
FT TER 124 124
SQ SEQUENCE 124 AA; 13440 MW; 33FF682A4C8E3862 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 124;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 104 VVLPAAEF 110

RESULT 170
Q9RJ45 PRELIMINARY; PRT; 124 AA.
ID Q9RJ45

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AC Q9RJ45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative integral membrane protein.
OX OFNames=SCI8.08C;
GN Streptomyces coelicolor.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939110; CAB59439.1; -
DR InterPro; IPR007436; DUF485.
DR Pfam; PF04341; DUF485; 1.
KW Complete proteome.
SQ SEQUENCE 124 AA; 13871 MW; A250973F80F3CFC CRC64;

Query Match 100.0%; Score 7; DB 2; Length 124;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 30 VQOAAEF 36

RESULT 171
SOR_ARCFU STANDARD; PRT; 125 AA.
ID SOR_ARCFU
AC Q29903;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative superoxide reductase (EC 1.15.1.2) (SOR).
GN OrderedLocusNames=AF0344;
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.P., McDonald L.A.,
RA Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -!- FUNCTION: Uses electrons from reduced NADP, by way of rubredoxin

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Qy	1	VXXXAEF 7
Dd	14	VDVFAEF 20
RESULT 173		
Q7R579	PRELIMINARY;	PRT; 126 AA.
ID Q7R579	AC Q7R579;	
DT 01-MAR-2004	(TrEMBLrel. 26, Created)	
DT 01-MAR-2004	(TrEMBLrel. 26, Last sequence update)	
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE GLP 587_95779_96159.		
OS Giardia_lambia ATCC 50803.		
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.		
OX NCBI_TaxID=184922;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=WB C6;		
RA Morrison H.G., McArthur A.G., Adam R.D., Alely S.B., Gillin F.D.,		
RA Olsen G.J., Sogin M.L.;		
ET "Draft sequence of the Giardia lamblia genome.";		
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.		
CC -! CAUTION: The sequence shown here is derived from an		
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is		
CC preliminary data.		
DR EMBL; AACB0100006; EAA42501.1; "-		
SQ SEQUENCE 126 AA; 13945 MW; 2BE6EEB9F73D7D7D CRC64;		
Query Match	100.0%; Score 7; DB 2; Length 126;	
Best Local Similarity	57.1%; Pred. No. 3.5e+03;	
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	VXXXAEF 7
Dd	90	VTAAEF 96
RESULT 174		
Q9XSf8	PRELIMINARY;	PRT; 126 AA.
ID Q9XSf8	AC Q9XSf8;	
DT 01-NOV-1999	(TrEMBLrel. 12, Created)	
DT 01-NOV-1999	(TrEMBLrel. 12, Last sequence update)	
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE MMP-7 protein (Fragment).		
OS Bos taurus (Bovine).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC Bovinae; Bos.		
OX NCBI_TaxID=9913;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=21071388; PubMed=11204721;		
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;		
RT "Coordinate expression of matrix-degrading proteinases and their		
ET activators and inhibitors in bovine skeletal muscle.";		
RL J. Anim. Sci. 79:94-107(2001).		
DR EMBL; AF135233; AAD30285.1; "-		
DR HSSP; P09237; LMWQ.		
DR MEROPS; M10.008; "-		
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.		
DR GO; GO:0004222; P:metalloendopeptidase activity; IEA.		
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR InterPro; IPR006026; Peptidase_M.		
DR InterPro; IPR001818; Pept_M10A_M12B.		
DR PRINTS; PR00138; MATRIXIN.		
DR SMART; SMO0235; ZnMc; 1.		
FT NON_TER 1		
FT NON_TER 126		
SQ SEQUENCE 126 AA; 13954 MW; E0EFC9B00F061653 CRC64;		

Query Match 100.0%; Score 7; DB 2; Length 126;
Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 1 VPVNAEF 7

RESULT 175
ACPS_SHEON STANDARD; PRT; 127 AA.
AC Q8EH77;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).

OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf K.M., Vamathevan J.J., Weidman J.F., Imbraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Knouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis";
RL Nat. Biotechnol. 20:1118-1123 (2002).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
family.

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CC -----
CC EMBL; A8015579; AAN54417.1; -;
CC HSSP; Q9F7T5; 1FTH.
CC TIGR; SO1352; -;
CC HMAP; MF 00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS_trans.
CC InterPro; IPR004568; Pantethn_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRFAMs; TIGR00516; acps; 1.
CC TIGRFAMs; TIGR00556; pantethn trn; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Magnesium; Transferase.
KW METAL 9 9 Magnesium (By similarity).
FT METAL 58 58 Magnesium (By similarity).
FT SEQUENCE 127 AA; 13638 MW; 6CA5CC686C50F2A0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 127;
Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 31 VLTEAEF 37

RESULT 176
Q6IGU8 PRELIMINARY; PRT; 127 AA.
AC Q6IGU8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HDC05167.

GN ORFNames=HDC05167;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP SEQUENCE FROM N.A.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohnselt J., Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:R3-R3 (2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC EMBL; BK003668; DAA02366.1; -;
DR EMBL; 127 AA; 14107 MW; 1195C1EBFA096D2 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 127;
Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:|:|:|
DB 21 VLISAEF 27

RESULT 177
Q73KS9 PRELIMINARY; PRT; 127 AA.
AC Q73KS9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ankyrin repeat protein.
GN OrderedLocusNames=TDE2138;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Teegaye G., Malek J.A., Ayodeji B.,
RA Shastan S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; A8017253; AAS12658.1; -;

RESULT 181

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=FG2077;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";
 RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL; AE017179; AA067038.1; -;
 DR TIGR; PG2077; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 128 AA; 13938 MW; EFECFBF299B464F CRC64;

Query Match 100.0%; Score 7; DB 2; Length 128;
 Best Local Similarity 57.1%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 58 VRSIAEF 64

RESULT 182

Q6HJDI PRELIMINARY; PRT; 128 AA.
 AC Q6HJDI
 DT 03-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BT9727.2016;
 OS Bacillus thuringiensis (Subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=180856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-27;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017355; AA759760.1; -;
 DR InterPro; IPR004360; Gly_bleo_diox.
 DR Pfam; PF00903; Glyoxalase; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 128 AA; 15000 MW; 0C91894404DBAF74 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 128;
 Best Local Similarity 57.1%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 77 VDEVAEF 83

RESULT 183

Q6LC16 PRELIMINARY; PRT; 128 AA.
 ID Q6LC16

AC Q6LC16;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Memory related protein-2 (Fragment).
 GN Names=MRG-2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=97420739; PubMed=9275181; DOI=10.1073/pnas.94.18.9669;
 RA Cavallaro S., Meiri N., Yi C.L., Musco S., Ma W., Goldberg J.,
 RA Alkon D.L.;
 RT "Late memory-related genes in the hippocampus revealed by RNA
 RT fingerprinting.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9669-9673(1997).
 DR EMBL; U95148; AAB70012.1; -;
 DR InterPro; IPR006096; GLFV_dehydrog_C.
 DR Pfam; PF02008; GLFV_dehydrog; 1.
 DR NON_TER 1
 FT SEQUENCE 128 AA; 14503 MW; 1292E523483008E7 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 128;

Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 57 VVPTAEF 63

RESULT 184

Q94MU0 PRELIMINARY; PRT; 129 AA.
 ID Q94MU0
 AC Q94MU0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P29.
 OS Bacteriophage Mx8.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC P22-like viruses.
 OX NCBI_TaxID=49964;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Youderian P., Walthers D., Salmi D., Magrini V., Hartzell P.L.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF396866; AAK94364.1; -;
 SQ SEQUENCE 129 AA; 14374 MW; FAA1BB6D82F54150 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 129;

Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
 |:::|
 DB 95 VERFAEF 101

RESULT 185

Q647R3 PRELIMINARY; PRT; 130 AA.
 ID Q647R3
 AC Q647R3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=GZ9D8_33;
 OS uncultured archaeon GZfos9D8.
 OC Archaea; environmental samples.

```

OX NCBI_TaxID=285401;
RN [1]_
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY174872; AAU84364.1; -.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 13385 MW; 66287CA77D2D3F74 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 111 VVTAEF 117
|::|||

RESULT 186
Q6C4P5 PRELIMINARY; PRT; 130 AA.
AC Q6C4P5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome E of strain CLIB99 of Yarrowia
DE lipolytica.
GN ORFNames=YALI0E24761g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CRG79966.1; -.
SQ SEQUENCE 130 AA; 14406 MW; 38939B0C71501B2A CRC64;

Query Match 100.0%; Score 7; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

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Db 33 VOQAEAF 39
|::|||

RESULT 187
Q6WIA2 PRELIMINARY; PRT; 130 AA.
AC Q6WIA2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=KVP40_0049;
OS Bacteriophage KVP40.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=75320;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22803260; PubMed=12923095;
RX DOI=10.1128/JB.185.17.5220-5233.2003;
RA Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A.,
RA Feldblyum T., White O., Paulsen I., Nierman W., Lee J.,
RA Szczypinski B., Fraser C.;
RT "Complete genome sequence of the broad-host-range vibriophage KVP40:
RT comparative genomics of a T4-related bacteriophage.";
RL J. Bacteriol. 185:5220-5233(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Miller E., Lee J., Szczypinski B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283928; AAQ64120.1; -.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 15375 MW; B09D64D376041759 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 50 VGKAEAF 56
|::|||

RESULT 188
Q84GF2 PRELIMINARY; PRT; 130 AA.
AC Q84GF2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OG Corynebacterium glutamicum (Brevibacterium flavum).
OC Plasmid pAG3.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=22220;
RX MEDLINE=22830013; PubMed=12948627; DOI=10.1016/S0168-1656(03)00157-3;
RA Tsuchi A., Puhler A., Kalinowski J., Thierbach G.;
RT "Plasmids in Corynebacterium glutamicum and their molecular
RT classification by comparative genomics.";
RL J. Biotechnol. 104:27-40(2003).
DR EMBL; AY172684; AAO18196.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 130 AA; 15205 MW; 353D203BB46A633 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7

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QY 1 VXXAAEF 7
RN 120 VQLLAEF 126
DB 120 VQLLAEF 126

RESULT 189
Q864Y6 PRELIMINARY; PRT; 131 AA.
AC Q864Y6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Small heat shock protein B3 (Fragment).
GN Name=hspb3;
OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Physeteridae; Physeter.
OX NCBI_TaxID=9755;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA de Jong W.W.; van Dijk M.A.M.; Foux C.; Kappe G.; van Rheede T.;
RA Madsen O.;
RT "Indels in protein-coding sequences of Euarchontoglires constrain the
RT rooting of the eutherian tree."
RL Mol. Phylogenet. Evol. 28:328-340(2003).
CC -1- SIMILARITY: Belongs to the small heat shock protein (HSP20)
CC family.
DR EMBL; AJ550775; CAD80062.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001436; Crystallin_alpha.
DR InterPro; IPR002068; Hsp20.
DR Pfam; PF00011; HSP20; 1.
DR PRINTS; PR00299; ACRYSTALLIN.
DR PROSITE; PS01031; HSP20; 1.
KW Heat shock.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14880 MW; 73DAD3252802CB CRC64;

Query Match 100.0%; Score 7; DB 2; Length 131;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
RN 6 VRYEAEF 12
DB 6 VRYEAEF 12

RESULT 190
Q9LQI6 PRELIMINARY; PRT; 131 AA.
AC Q9LQI6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE F28G4.20 protein (Hypothetical protein).
GN Name=F28G4.20;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A.; Palm C.J.; Conway A.B.; Conn L.; Hansen N.F.;
RA Altafi H.; Nguyen M.; Lam B.; Southwick A.; Miranda M.; Brooks S.;
RA Buehler E.; Chao Q.; Chin C.; Chiou J.; Choi E.; Gonzalez A.;
RA Hwang B.; Johnson-Hopson C.; Khan S.; Kim C.; Koo T.; Lee J.M.;
RA Lenz C.; Liu A.; Liu S.; Mukharsky N.; Pham P.; Sakano H.; Shinn P.;
RA Toriumi M.; Vaysberg M.; Yu G.; Ecker J.; Theologis A.; Davis R.W.;
```

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RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Seki M.; Iida K.; Satou M.; Sakurai T.; Akiyama K.; Ishida J.;
RA Nakajima M.; Enju A.; Kamiya A.; Narusaka M.; Carninci P.; Kawai J.;
RA Hayashizaki Y.; Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007843; AAF97310.1; -.
DR EMBL; AK118889; BAC43474.1; -.
DR PIR; A86310; A86310. Auxin inducible.
DR InterPro; IPR003676; Auxin inducible.
DR Pfam; PF02519; Auxin inducible; 1.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 15084 MW; DB1CA4A8AE1742C CRC64;

Query Match 100.0%; Score 7; DB 2; Length 131;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
RN 122 VEELAEF 128
DB 122 VEELAEF 128

RESULT 191
Q55519 PRELIMINARY; PRT; 131 AA.
AC Q55519;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S110525 protein.
GN OrderedLocustNames=s110525;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC6803;
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T.; Sato S.; Kotani H.; Tanaka A.; Asamizu E.; Nakamura Y.;
RA Miyajima N.; Hiroseawa M.; Sugiyama M.; Sasamoto S.; Kimura T.;
RA Hosouchi T.; Matsuno A.; Muraki A.; Nakazaki N.; Naruo K.; Okumura S.;
RA Shimpo S.; Takeuchi C.; Wada T.; Watanabe A.; Yamada M.; Yasuda M.;
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
DR EMBL; D64006; BAA10878.1; -.
DR PIR; S76031; S76031.
DR InterPro; IPR002716; P1LT_N.
DR Pfam; PF01850; PIN; 1.
KW Complete proteome.
SQ SEQUENCE 131 AA; 15113 MW; 4D4A19D6018941A4 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 131;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
RN 69 VKLGAEF 75
DB 69 VKLGAEF 75

RESULT 192
RNPA MICLU STANDARD; PRT; 132 AA.
AC P21172;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNasep protein) (RNase
```

DE P protein) (Protein C5).
GN Name: rnpA;
OC Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococaceae; Micrococaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91033019; PubMed=2172090; DOI=10.1016/0378-1119(90)90138-H;
RA Fujita M.Q., Yoshikawa H., Ogasawara N.;
RT "Structure of the dnaA region of Micrococcus luteus: conservation and
RT variations among eubacteria.";
RL Gene 93.73-78(1990).
CC -!- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5'terminus. It can also cleave
CC other RNA substrates such as 4.5S RNA. The protein component plays
CC an auxiliary but essential role in vivo by binding to the 5'-
CC leader sequence and broadening the substrate specificity of the
CC ribozyme (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extranucleotide from tRNA precursor.
CC -!- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (By similarity).
CC -!- SIMILARITY: Belongs to the rnpA family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34006; AAA25313.1; -.
DR PIR; JQ0737; JQ0737.
DR HAMAP; MF_00227; -; 1.
DR InterPro; IPR000100; Ribonuclease_P.
DR Pfam; PF00825; Ribonuclease_P; 1.
DR ProDom; PD003629; Ribonuclease_P; 1.
DR TIGRFAMs; TIGR00188; rnpA; 1.
DR PROSITE; PS00648; RIBONUCLEASE_P; 1.
KW Endonuclease; Hydrolase; Nuclease; RNA-binding; tRNA processing.
SQ SEQUENCE 132 AA; 14408 MW; E7E29CEA67BPAc13 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 132;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
DB 8 VRTPAEF 14

RESULT 193
Q9HHU1 ID Q9HHU1 PRELIMINARY; PRT; 132 AA.
AC Q9HHU1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vng6226h.
DE OrderedLocusNames=VNG6226H;
GN Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OG Plasmid pNRC200.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005156; AAG20885.1; -.
KW Complete proteome; Plasmid.
SQ SEQUENCE 132 AA; 14319 MW; EF0CA56BDA7C4CB1 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
DB 80 VAQAEAF 86

RESULT 194
Q836D9 ID Q836D9 PRELIMINARY; PRT; 132 AA.
AC Q836D9
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycerol-3-phosphate cytidyltransferase.
GN Name=gct; OrderedLocusNames=EFl175;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerji L., Myers G.S.A., Nelson K.E., Sehadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis";
RL Science 299:2071-2074(2003).
DR EMBL; AE016950; AA080975.1; -.
DR HSSP; P27623; LCOZ.
DR TIGR; EF1175; -.
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0047348; F:glycerol-3-phosphate cytidyltransferase a. . .; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0019350; P:teichoic acid biosynthesis; IEA.
DR InterPro; IPR004820; Cytidylyltransf.
DR InterPro; IPR004821; Cyt trans. rel.
DR Pfam; PF01467; CTP transf. 2; 1.
DR TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
DR TIGRFAMs; TIGR01518; g3p_cytidylytns; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 132 AA; 15440 MW; 223B4D8A9A5DF98F CRC64;

Query Match 100.0%; Score 7; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
|:::|
DB 78 VSDIAEF 84

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RESULT 195
Q8XQ26 PRELIMINARY; PRT; 133 AA.
AC Q8XQ26;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein RSP1072.
GN Name=RS02541; OrderedLocusNames=RSPl072;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21691879; PubMed=11923852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA Siguer P., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002)
DR EMBL; AL646082; CAD18223.1; -;
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 133 AA; 15279 MW; 885E27C306BB8619 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 133;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 62 VTGAEF 68

RESULT 196
Q7UBX5 PRELIMINARY; PRT; 133 AA.
AC Q7UBX5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=S2796;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016987; AAP17944.1; -;
KW Hypothetical protein.
SQ SEQUENCE 133 AA; 14695 MW; D4AD081ED70570F3 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 133;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 62 VTGAEF 68

RESULT 197
YK49_STRCO STANDARD; PRT; 134 AA.
ID YK49_STRCO
AC P16251; Q9S2T6;
DT 01-AUG-1990 (Rel. 15, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein SCO2049.
GN OrderedLocusNames=SCO2049; ORFNames=SC4G6.18c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)";
RL Nature 417:141-147(2002).
RN [2]
RP SEQUENCE OF 1-76 FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=90337345; PubMed=2199329; DOI=10.1016/0378-1119(90)90436-U;
RA Limauro D., Avitabile A., Cappellano M., Puglia A.M., Bruni C.B.;
RT "Cloning and characterization of the histidine biosynthetic gene
cluster of Streptomyces coelicolor A3(2).";
RL Gene 90:31-41(1990).
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CC -----
CC EMBL; AL939111; CAB51441.1; -;
CC DR EMBL; M31628; AAA26761.1; -;
CC DR PIR; PQ0113; PQ0113.
CC DR PIR; T35078; T35078.
CC DR InterPro; IPR006175; Endoribon_LSPS.
CC DR Pfam; PF01042; Ribonuc_L-PS; 1.
CC KW Complete proteome; Hypothetical protein.
CC FT CONFLICT 49 49 D -> P (in Ref. 2).
CC SQ SEQUENCE 134 AA; 14382 MW; F3ECA6F393A7814B CRC64;

Query Match 100.0%; Score 7; DB 1; Length 134;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
Db 62 VEAIAEF 68

RESULT 198
Q6MKI1 PRELIMINARY; PRT; 134 AA.
ID Q6MKI1
AC Q6MKI1;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemotaxis response regulator CheY.
GN Names=CheY; OrderedLocusNames=Bd2409;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842652; CAE80226.1; -.
DR HSSP; P06143; 1AB6.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:000156; F:two-component response regulator activity; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR011006; CheY_like.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.
KW Complete proteome; Phosphorylation; Sensory transduction.
SQ SEQUENCE 134 AA; 15035 MW; A76AF72470EA59EF CRC64;

Query Match 100.0%; Score 7; DB 2; Length 134;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 77 VRATAEF 83

RESULT 199
YE49_CAMJE STANDARD; PRT; 135 AA.
AC Q9PML1;
CT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical UPF0306 protein Cj1449c.
GN OrderedLocusNames=Cj1449c;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Kariyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -!- SIMILARITY: Belongs to the UPF0306 family.
CC
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DR EMBL; AL139078; CAB73872.1; -.
DR FIR; H81290; H81290.
DR HAMAP; MF_00764; -.
DR InterPro; IPR011194; DUF UCP009554.
DR InterPro; IPR009002; FMN_binding.
DR PIRSF; PIRSF009554; UCP009554; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 135 AA; 15640 MW; A6201FD0DAAE284B CRC64;

Query Match 100.0%; Score 7; DB 1; Length 135;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 77 VOAKAEF 83

RESULT 200
Q8ZVC6 PRELIMINARY; PRT; 135 AA.
AC Q8ZVC6;
CT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE2350.
GN OrderedLocusNames=PAE2350;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009871; AAL64130.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 135 AA; 15043 MW; A1DBFBD4D0DD79BD CRC64;

Query Match 100.0%; Score 7; DB 2; Length 135;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VXXAAEF 7
DB 70 VERYAEF 76

Search completed: November 15, 2005, 10:59:36
Job time : 124 secs

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